Cook, L.
09/627383

FILE 'REGISTRY' ENTERED AT 15:39:03 ON 07 JUN 2002
L1 28 S LEPRAS/SQSP

Seq. ID 1

FILE 'HCAPLUS' ENTERED AT 15:40:09 ON 07 JUN 2002
L2 23 S L1

L2 ANSWER 1 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:872087 HCAPLUS
DOCUMENT NUMBER: 136:227947
TITLE: Nucleic acids and their encoded polypeptides from human tissues
INVENTOR(S): Tang, Y. Tom; Liu, Chenghua; Drmanac, Radoje T.
PATENT ASSIGNEE(S): Hyseq, Inc., USA
SOURCE: PCT Int. Appl., 831 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 65
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001088088	A2	20011122	WO 2001-XC14827	20010516
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001088088	A2	20011122	WO 2001-US14827	20010516
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.: US 2000-577408 A 20000518
WO 2001-US14827 W 20010516

AB The present invention provides a collection or library of 8051 nucleic acid contig sequences assembled from expressed sequence tag or cDNA libraries isolated mainly by sequencing by hybridization (SBH), std. PCR, Sanger sequencing techniques, and in some cases, sequences obtained form one or more public databases. The cDNA libraries are from human tissue sources and nearest neighbor sequence homologies are provided. The invention also relates to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. [This abstr. record is one of four records for this

document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **403520-71-8 403546-70-3**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acids and their encoded polypeptides from human tissues)

L2 ANSWER 2 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:798430 HCAPLUS
DOCUMENT NUMBER: 135:353807
TITLE: Propionibacterium acnes nucleic acids and proteins useful for therapy and diagnosis of acne vulgaris
INVENTOR(S): Skeiky, Yasir A. W.; Persing, David H.; Mitcham, Jennifer L.; Wang, Siqing Steven; Bhatia, Ajay; L'Maisonneuve, Jean-Francois; Zhang, Yanni; Jen, Shyian; Carter, Darrick
PATENT ASSIGNEE(S): Corixa Corporation, USA
SOURCE: PCT Int. Appl., 1069 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001081581	A2	20011101	WO 2001-US12865	20010420
WO 2001081581	A3	20020314		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001081581	A2	20011101	WO 2001-XA12865	20010420
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001081581	A2	20011101	WO 2001-XB12865	20010420
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,				

LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

WO 2001081581 A2 20011101 WO 2001-XC12865 20010420

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

WO 2001081581 A2 20011101 WO 2001-XD12865 20010420

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

WO 2001081581 A2 20011101 WO 2001-XE12865 20010420

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-199047P P 20000421
US 2000-208841P P 20000602
US 2000-216747P P 20000707
WO 2001-US12865 W 20010420

AB Compns. and methods for the therapy and diagnosis of acne vulgaris and other related conditions are disclosed. Compns. may comprise one or more Propionibacterium acnes proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Thus, overlapping clones representing .apprx.8.6 full-length genome equiv. from a P. acnes genomic library were aligned to form 299 linear contigs. These 299 contigs represent a total assembled length of about 2,656,860 nucleotides covering >90% of the P. acnes genome. Six-frame translation is performed in order to predict 28,913 open reading frames encoding P. acnes polypeptide sequences .gtoreq.50

amino acids in length. A therapeutic compn. may also comprise an antibody that binds a P. acnes protein, antigen-presenting cells that express a P. acnes protein, or a T cell that is specific for cells expressing such a protein. Such compns. may be used, for example, for the prevention and/or treatment of acne. [This abstr. record is the first of six records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **371995-57-2**
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; Propionibacterium acnes nucleic acids and proteins useful for therapy and diagnosis of acne vulgaris)

L2 ANSWER 3 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:781083 HCAPLUS
DOCUMENT NUMBER: 135:353783
TITLE: Human nucleic acids and their encoded polypeptides
INVENTOR(S): Tang, Y. Tom; Liu, Chenghua; Drmanac, Radoje T.
PATENT ASSIGNEE(S): Hyseq, Inc., USA
SOURCE: PCT Int. Appl., 765 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 65
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001079449	A2	20011025	WO 2001-US8656	20010416
WO 2001079449	A3	20020328		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-552929 A 20000418
US 2001-770160 A 20010126

AB The present invention provides 5497 novel nucleic acids, 5497 novel polypeptide sequences encoded by these nucleic acids, and their uses for diagnostic, therapeutic, and research purposes. A collection or library of the novel nucleic acid sequences were assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization, and in some cases, sequences obtained from one or more public databases. Contigs were assembled using the EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling addnl. sequences from different databases that belong to this assemblage. [This abstr. record is one of two records for this document

necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **369659-63-2P**
RL: ANT (Analyte); BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; human nucleic acids and their encoded polypeptides)

L2 ANSWER 4 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:545709 HCAPLUS
DOCUMENT NUMBER: 135:148240
TITLE: Human nucleic acids and polypeptides
INVENTOR(S): Tang, Y. Tom; Liu, Chenghua; Asundi, Vinod; Chen, Rui-hong; Ma, Yunqing; Qian, Xiaohong B.; Ren, Feiyan; Wang, Dunrui; Wang, Jian-rui; Wang, Zhiwei; Wehrman, Tom; Xu, Chongjun; Xue, Aidong J.; Yang, Yonghong; Zhang, Jie; Zhao, Qing A.; Zhou, Ping; Goodrich, Ryle; Drmanac, Radoje T.
PATENT ASSIGNEE(S): Hyseq, Inc., USA; et al.
SOURCE: PCT Int. Appl., 10078 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 65
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001053312	A1	20010726	WO 2000-US34263	20001226
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001025965	A5	20010731	AU 2001-25965	20001222

PRIORITY APPLN. INFO.:

US 2000-488725	A	20000121
US 2000-552317	A	20000425
US 2000-598042	A	20000709
US 2000-620312	A	20000719
US 2000-653450	A	20000803
US 2000-662191	A	20000915
US 2000-693036	A	20001019
US 2000-727344	A	20001129
US 1999-471275	A	19991223
WO 2000-US35190	W	20001222

AB The present invention provides 1768 novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids, and uses thereof. A plurality of novel nucleic acids were obtained from cDNA libraries prepd. from various human tissues and in some cases from a

genomic library derived from human chromosomes using std. PCR, sequencing by hybridization (SBH) sequence signature anal., and Sanger sequencing techniques. The contigs or nucleic acids of the present invention were assembled using an EST sequence as a seed, with a recursive algorithm used to extend the seed EST into an extended assemblage by pulling addnl. sequences from different databases that belong to this assemblage. Full-length gene cDNA sequences and their corresponding protein sequences were generated from the assemblage.

IT **352374-90-4 352374-91-5 352374-92-6**
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; human nucleic acids and polypeptides)

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 5 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:241691 HCAPLUS
DOCUMENT NUMBER: 134:261275
TITLE: Use of a BMP protein receptor complex for screening bone metabolism actives and cells co-transfected with a type II BMP receptor and type I BMP receptor
INVENTOR(S): Rosenbaum, Jan Susan
PATENT ASSIGNEE(S): The Procter & Gamble Company, USA
SOURCE: U.S., 85 pp., Cont.-in-part of U.S. Ser. No. 334,178, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6210899	B1	20010403	US 1995-462467	19950605
WO 9614579	A1	19960517	WO 1995-US14027	19951030
W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9539713	A1	19960531	AU 1995-39713	19951030
AU 710559	B2	19990923		
EP 789844	A1	19970820	EP 1995-937676	19951030
EP 789844	B1	20020206		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, PT, SE				
JP 10510047	T2	19980929	JP 1995-515373	19951030
AT 213064	E	20020215	AT 1995-937676	19951030

PRIORITY APPLN. INFO.: US 1994-334178 B2 19941104
US 1995-462467 A 19950605
WO 1995-US14027 W 19951030

AB The present invention relates to a method for detg. whether a compd.

is capable of binding to a BMP receptor kinase protein complex. The invention further relates to a method for detg. the concn. of a BMP receptor ligand in a clin. sample. The invention also relates to a host cell co-transfected with an expression vector comprising a DNA sequence that codes for the BMP receptor kinase protein BRK-3 and an expression vector comprising a DNA sequence that codes for a BMP type I receptor kinase protein. The invention further relates to a host cell co-transfected with an expression vector comprising a DNA sequence that codes for a sol. or incomplete BMP type I receptor kinase protein and a sol. or incomplete BMP receptor kinase protein BRK-3. The invention further relates to a method for detg. whether a test compd. produces a signal upon binding to a BMP receptor protein complex.

IT **332001-59-9P 332001-60-2P**
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; use of BMP protein receptor complex for screening bone metab. actives and cells co-transfected with type II BMP receptor and type I BMP receptor)

REFERENCE COUNT: 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 6 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:208400 HCAPLUS
DOCUMENT NUMBER: 134:248841
TITLE: Crystalline three-dimensional structure of a metallo .beta.-lactamase IMP-1 from Pseudomonas aeruginosa and its complex with the inhibitor SB-252619, and applications to drug design
INVENTOR(S): Abdel-Meguid, Sherin S.; Concha, Nestor O.
PATENT ASSIGNEE(S): SmithKline Beecham Corporation, USA
SOURCE: PCT Int. Appl., 243 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001019971	A1	20010322	WO 2000-US25340	20000915

W: CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.: US 1999-154749P P 19990917

AB Native crystal structure of a novel Pseudomonas aeruginosa metallo .beta.-lactamase IMP-1 and crystal structure of the P. aeruginosa metallo .beta.-lactamase IMP-1 complexed with the inhibitor SB-252619 are disclosed. The invention provides direct information on the specific role of the residues in the active site responsible for the binding of inhibitors, substrates and substrate analogs. This information could be used in search for new antibacterial drugs and in designing drugs useful for inhibiting the P. aeruginosa .beta.-lactamase IMP-1.

IT **331287-05-9**
RL: PRP (Properties)

(unclaimed protein sequence; cryst. three-dimensional structure of a metallo .beta.-lactamase IMP-1 from Pseudomonas aeruginosa and its complex with the inhibitor SB-252619, and applications to drug design)

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:125385 HCAPLUS
DOCUMENT NUMBER: 135:15597
TITLE: Molecular and functional characterization of a family of rat brain T-type calcium channels
AUTHOR(S): McRory, John E.; Santi, Celia M.; Hamming, Kevin S. C.; Mezeyova, Janette; Sutton, Kathy G.; Baillie, David L.; Stea, Anthony; Snutch, Terrance P.
CORPORATE SOURCE: Biotechnology Laboratory, University of British Columbia, Vancouver, BC, V6T 1Z3, Can.
SOURCE: Journal of Biological Chemistry (2001), 276(6), 3999-4011
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Voltage-gated calcium channels represent a heterogeneous family of calcium-selective channels that can be distinguished by their mol., electrophysiol., and pharmacol. characteristics. We report here the mol. cloning and functional expression of three members of the low voltage-activated calcium channel family from rat brain (.alpha.1G, .alpha.1H, and .alpha.1I). Northern blot and reverse transcriptase-polymerase chain reaction analyses show .alpha.1G, .alpha.1H, and .alpha.1I to be expressed throughout the newborn and juvenile rat brain. In contrast, while .alpha.1G and .alpha.1H mRNA are expressed in all regions in adult rat brain, .alpha.1I mRNA expression is restricted to the striatum. Expression of .alpha.1G, .alpha.1H, and .alpha.1I subunits in HEK293 cells resulted in calcium currents with typical T-type channel characteristics: low voltage activation, neg. steady-state inactivation, strongly voltage-dependent activation and inactivation, and slow deactivation. In addn., the direct electrophysiol. comparison of .alpha.1G, .alpha.1H, and .alpha.1I under identical recording conditions also identified unique characteristics including activation and inactivation kinetics and permeability to divalent cations. Simulation of .alpha.1G, .alpha.1H, and .alpha.1I T-type channels in a thalamic neuron model cell produced unique firing patterns (burst vs. tonic) typical of different brain nuclei and suggests that the three channel types make distinct contributions to neuronal physiol.

IT **342874-40-2**
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
(amino acid sequence; cloning, sequence and characterization of a family of rat brain T-type calcium channels)

REFERENCE COUNT: 58 THERE ARE 58 CITED REFERENCES AVAILABLE

FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 8 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:106055 HCAPLUS
DOCUMENT NUMBER: 134:188985
TITLE: Human expressed sequence tags and primers for synthesizing full-length cDNAs
INVENTOR(S): Ota, Toshio; Isogai, Takao; Nishikawa, Tetsuo; Hayashi, Kohji; Saito, Kaoru; Yamamoto, Junichi; Ishii, Shizuko; Sugiyama, Tomoyasu; Wakamatsu, Ai; Nagai, Keiichi; Otsuki, Tetsuji
PATENT ASSIGNEE(S): Helix Research Institute, Japan
SOURCE: Eur. Pat. Appl., 2527 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 9
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1074617	A2	20010207	EP 2000-116126	20000728
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1205549	A1	20020515	EP 2000-948282	20000728
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				

PRIORITY APPLN. INFO.:

JP 1999-248036	A	19990729
JP 1999-300253	A	19990827
JP 2000-118776	A	20000111
JP 2000-183767	A	20000502
JP 2000-241899	A	20000609
US 1999-159590P	P	19991018
US 2000-183322P	P	20000217
WO 2000-JP5065	W	20000728

AB Primers for synthesizing full-length cDNAs and their use are provided. The invention provides 5'-end sequences for 5602 partial cDNA sequences (expressed sequence tags, ESTs) and 3'-end sequences for 4970 of these clones. Furthermore, primers for synthesizing the full-length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full-length cDNA sequences s of the present invention contg. the translation start site provides information useful for analyzing the functions of the proteins. Tissue- and cell-specific expression patterns are also provided. [This abstr. record is one of 6 records for this patent necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **326928-35-2**, Protein (human clone PLACE1004777)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; human expressed sequence tags and primers for synthesizing full-length cDNAs)

L2 ANSWER 9 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:101181 HCAPLUS
DOCUMENT NUMBER: 134:159864
TITLE: Affinity fluorescent proteins and uses for

ligand detection
INVENTOR(S): Matsudaira, Paul T.; Ehrlich, Daniel J.; Zhong, Qiuhui; Freyson, Yelena
PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA
SOURCE: PCT Int. Appl., 44 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001009177	A2	20010208	WO 2000-US20619	20000728

W: CA, JP
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRIORITY APPLN. INFO.: US 1999-146438P P 19990729

AB The present invention is related to an affinity fluorescent protein (aFP) comprising a modified fluorescent protein or mol. which comprises a heterologous amino acid sequence, thereby introducing a ligand-activated protein binding site. The modified fluorescent protein displays an altered spectral property when the binding site is engaged with ligand relative to the spectral property displayed when the binding site is not engaged by ligand. The hexapeptide Leu-Glu-Pro-Arg-Ala-Ser which contains 3 restriction enzyme sites (XhoI-AvrI-NheI) is useful for identifying fluorescent insensitive sites in the green fluorescent protein (GFP). An epitope from hemagglutinin (HA tag comprising Tyr-Pro-Tyr-Asp-Val-Pro-Asp-Tyr-Ala) that is recognized by the monoclonal antibody 12CA5 is inserted into between residues Gln157-Lys158 and/or Glu172-Asp173 and/or at the C-terminus of GFP; a Ser-147-Pro substitution is introduced into GFP for improved stability. The present invention also relates to an aFP expression cassette comprising a modified fluorescent protein nucleic acid sequence operatively linked to expression control sequences, wherein the modified fluorescent protein sequence comprises a recombinant peptide which comprises restriction endonuclease sites. The present invention also relates to a method of detecting the presence of a target ligand in a mixt. of macromols. Also encompassed by the present invention is a method of detecting the occurrence of a target ligand in a cell (e.g., a macrophage, a yeast cell).

IT **324745-26-8**
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(affinity ligand; affinity fluorescent proteins and uses for ligand detection)

L2 ANSWER 10 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:56134 HCAPLUS
DOCUMENT NUMBER: 135:176236
TITLE: Cloning and structural characterization of ECTACC, a new member of the transforming acidic coiled coil (TACC) gene family: cDNA sequence and expression analysis in human microvascular endothelial cells
AUTHOR(S): Pu, Jeffrey J.; Li, Chaoyang; Rodriguez, Marilis; Banerjee, Debendranath

CORPORATE SOURCE: Department of Membrane Biochemistry II, The Lindsley F. Kimball Research Institute, New York Blood Center, New York, NY, 10021, USA
SOURCE: Cytokine (2001), 13(3), 129-137
CODEN: CYTIE9; ISSN: 1043-4666
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Erythropoietin (Epo) transduces mitogenic and chemoattractant signals to human endothelial cells. Identifications of Epo-responsive genes are important for understanding the mol. nature of Epo signaling in endothelial cells. The effects of Epo on differential expression of various genes were examd. in human microvascular endothelial cells (HMVEC) by differential display reverse transcriptase polymerase chain reaction (RT-PCR). In the current study we obtained from Epo-treated HMVEC a cDNA fragment with characteristics of the 3' end of mRNA. Using the cDNA fragment, we then selectively isolated a full-length clone by screening an unamplified endothelial cell cDNA library followed by 5' rapid amplification of cDNA ends by polymerase chain reaction (RACE-PCR). The nucleotide sequence of the longest cDNA revealed an open reading frame of 3311 nucleotides that encodes a protein consisting of .apprx.906 amino acids with a predicted MW of .apprx.100 kDa. The nucleotide sequence of the cDNA is nearly identical to that of transforming acidic coiled coil-contg. (TACC2) and anti-zuai-1 (AZU-1) cDNA clones except at the 5'- and 3'-ends. Northern blot anal. showed an increase in endothelial-TACC-related mRNA levels in Epo-treated cells in comparison to that of the control cells. Endothelial-TACC-related mRNA was highly expressed in heart and skeletal muscle tissue. Placenta and brain tissue exhibited low levels of expression of endothelial-TACC-related gene. Southern blot anal. of genomic DNA from somatic cell hybrids showed that endothelial-TACC-related cDNA maps to chromosome 10. Immunofluorescence microscopy and the occurrence of several putative phosphorylation and SH3 binding sites on the deduced protein suggest that endothelial-TACC-related protein may be involved in Epo signaling cascades in endothelial cells. (c) 2001 Academic Press.

IT **355157-34-5**, Protein ECTACC (human)
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(amino acid sequence; cloning and structural characterization of ECTACC of human, a new member of the transforming acidic coiled coil (TACC) gene family)

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 11 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:31638 HCAPLUS
DOCUMENT NUMBER: 134:111253
TITLE: Novel mammalian calcium channels and related probes, cell lines and methods
INVENTOR(S): Snutch, Terrance P.; Baillie, David L.
PATENT ASSIGNEE(S): Neuromed Technologies, Inc., Can.
SOURCE: PCT Int. Appl., 103 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001002561	A2	20010111	WO 2000-CA794	20000704
WO 2001002561	A3	20010628		
W: AU, CA, IL, JP, NO, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 1190053	A2	20020327	EP 2000-945479	20000704
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1999-346794 A 19990702
WO 2000-CA794 W 20000704

AB Sequences and partial sequences for three types of mammalian (human and rat sequences identified) T-type calcium channel subunits which we have labeled as the .alpha.1G, .alpha.1H and .alpha.1I subunits are provided. Knowledge of the sequence of these calcium channels permits the localization and recovery of the complete sequence from human cells, and the development of cell lines which express the novel calcium channels of the invention. These cells may be used for identifying compds. capable of acting as agonists or antagonists to the calcium channels.

IT **319502-44-8**
RL: PRP (Properties)
(unclaimed protein sequence; novel mammalian calcium channels and related probes, cell lines and methods)

L2 ANSWER 12 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:12616 HCAPLUS
DOCUMENT NUMBER: 134:82484
TITLE: Fanconi anemia protein interacting proteins FANCIP2 and FANCIP3 and cDNAs and methods for diagnosis and treatment of diseases
INVENTOR(S): Gross, Hans Joachim; Reuter, Tanja; Hanenberg, Helmut; Herterich, Sabine; Wagner, Matthias
PATENT ASSIGNEE(S): Multigene Biotech Gmbh, Germany
SOURCE: PCT Int. Appl., 60 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001000822	A2	20010104	WO 2000-EP5878	20000626
WO 2001000822	A3	20010705		
W: AE, AL, AM, AU, AZ, BA, BB, BG, BR, BY, CA, CN, CR, CU, CZ, DM, EE, GD, GE, HR, HU, ID, IL, IN, IS, JP, KG, KP, KR, KZ, LC, LK, LR, LT, LV, MA, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, TT, TZ, UA, US, UZ, VN, YU, ZA				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
DE 19929887	A1	20010111	DE 1999-19929887	19990629
EP 1194547	A2	20020410	EP 2000-943885	20000626

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.: DE 1999-19929887 A 19990629
WO 2000-EP5878 W 20000626

AB The invention relates to cDNA sequences encoding proteins FANCIP2 and FANCIP3, which interact with the Fanconi anemia complementation group A (FANCA) protein, and the corresponding encoded proteins. The invention also relates to antibodies directed to said proteins, to FANCIP2- or FANCIP3-transgenic organisms and cells, and to the use of FANCIP2 and FANCIP3 for effector screening, and to the pharmaceutical application of the inventive nucleic acids, proteins and antibodies.

IT **316927-56-7**
RL: PRP (Properties)
(unclaimed protein sequence; fanconi anemia protein interacting proteins FANCIP2 and FANCIP3 and cDNAs and methods for diagnosis and treatment of diseases)

L2 ANSWER 13 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:540554 HCAPLUS
DOCUMENT NUMBER: 133:130477
TITLE: The genome sequence of the plant pathogen Xylella fastidiosa
AUTHOR(S): Simpson, A. J. G.; Reinach, F. C.; Arruda, P.; Abreu, F. A.; Acencio, M.; Alvarenga, R.; Alves, L. M. C.; Araya, J. E.; Bala, G. S.; Baptista, C. S.; Barros, M. H.; Bonaccorsi, E. D.; Bordin, S.; Bove, J. M.; Briones, M. R. S.; Bueno, M. R. P.; Camargo, A. A.; Camargo, L. E. A.; Carraro, D. M.; Carrer, H.; Colauto, N. B.; Colombo, C.; Costa, F. F.; Costa, M. C. R.; Costa-Neto, C. M.; Coutinho, L. L.; Cristofani, M.; Dias-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A. P.; Ferreira, A. J. S.; Ferreira, V. C. A.; Ferro, J. A.; Fraga, J. S.; Franca, S. C.; Franco, M. C.; Frohme, M.; Furtan, L. R.; Garnier, M.; Goldman, G. H.; Goldman, M. H. S.; Gomes, S. L.; Gruber, A.; Ho, P. L.; Hoheisel, J. D.; Junqueira, M. L.; Kemper, E. L.; Kitajima, J. P.; Kreiger, J. E.; Duramae, E. E.; Laigret, F.; Lambals, M. R.; Lette, L. C. C.; Lemos, E. G. M.; Lemos, M. V. F.; Lopes, S. A.; Lopes, C. R.; Machado, J. A.; Machado, M. A.; Madeira, A. M. B. N.; Madeira, H. M. F.; Marino, C. L.; Marques, M. V.; Martins, E. A. L.; Martins, E. M. F.; Matsukuma, A. Y.; Menck, C. F. M.; Miracca, E. C.; Miyaki, C. Y.; Monteiro-Vitorello, C. B.; Moon, D. H.; Nagai, M. A.; Nascimento, A. L. T. O.; Netto, L. E. S.; Nhanl, A., Jr.; Nobrega, F. G.; Nunes, L. R.; Oliveira, M. A.; de Oilveria, M. C.; de Oliveira, R. C.; Palmieri, D. A.; Paris, A.; Peixoto, B. R.; Pereira, G. A. G.; Perelra, H. A.; Pesquero, J. B.; Quaggio, R. B.; Roberto, P. G.; Rodrigues, V.; Rosa, A. J. de M.; de Rosa, V. E., Jr.; de Sa, R. G.; Santelli, R. V.; Sawasaki, H. E.; da Silva, A. C. R.; da Silva, A. M.; da Silva, F. R.; Silva, W. A., Jr.; da

Silveira, J. F.; Silvestri, M. L. Z.; Siqueira, W. J.; de Souza, A. A.; de Souza, A. P.; Terenzi, M. F.; Truffi, D.; Tsai, S. M.; Tsuhako, M. H.; Vallada, H.; Van Sluys, M. A.; Verjovski-Almeida, S.; Vettore, A. L.; Zago, M. A.; Zatz, M.; Meidanis, J.; Setubal, J. C.

CORPORATE SOURCE: Instituo Ludwig de Pesquisa sobre o Cancer, Sao Paulo, 01509-010, Brazil

SOURCE: Nature (London) (2000), 406(6792), 151-157
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Xylella fastidiosa is a fastidious, xylem-limited bacterium that causes a range of economically important plant diseases. The complete genome sequence of X. fastidiosa clone 9a5c, which causes citrus variegated chlorosis-a serious disease of orange trees, is reported. The genome comprises a 52.7% GC-rich 2,679,305-base-pair (bp) circular chromosome and two plasmids of 51,158 bp and 1,285 bp. Putative functions can be assigned to 47% of the 2904 predicted coding regions. Efficient metabolic functions are predicted, with sugars as the principal energy and carbon source, supporting existence in the nutrient-poor xylem sap. The mechanisms assocd. with pathogenicity and virulence involve toxins, antibiotics and ion sequestration systems, as well as bacterium-bacterium and bacterium-host interactions mediated by a range of proteins. Orthologs of some of these proteins have only been identified in animal and human pathogens; their presence in X. fastidiosa indicates that the mol. basis for bacterial pathogenicity is both conserved and independent of host. At least 83 genes are bacteriophage-derived and include virulence-assocd. genes from other bacteria, providing direct evidence of phage-mediated horizontal gene transfer.

IT **284706-28-1**, Protein (Xylella fastidiosa gene XF1737)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of the plant pathogen Xylella fastidiosa)

L2 ANSWER 14 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:246921 HCAPLUS
DOCUMENT NUMBER: 132:275067
TITLE: The genome sequence of Drosophila melanogaster
AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu,

Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene

W.; Rubin, Gerald M.; Venter, J. Craig
CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA
SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was detd. of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstr. record is one of 4 records for this document necessitated by the large no. of index entries required to fully index the document and publication system restraints.].

IT **263525-23-1**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Drosophila melanogaster)

L2 ANSWER 15 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:230405 HCAPLUS
DOCUMENT NUMBER: 132:304167
TITLE: The genome sequence of Drosophila melanogaster
AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter;

Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLleod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA

SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The fly Drosophila melanogaster is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was detd. of nearly all of the .apprx.120-megabase euchromatic portion of the Drosophila genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller Caenorhabditis elegans genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at http://flybase.bio.indiana.edu and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstr. record is one of 4 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].
IT **262988-39-6**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of Drosophila melanogaster)
REFERENCE COUNT: 89 THERE ARE 89 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 16 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:161309 HCAPLUS
DOCUMENT NUMBER: 132:204089
TITLE: Protein and cDNA sequences encoding Neisseria meningitidis NMASP protein, and uses thereof in treating meningitis
INVENTOR(S): Jackson, W. James; Harris, Andrea M.
PATENT ASSIGNEE(S): Antex Biologics Inc., USA
SOURCE: PCT Int. Appl., 76 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000012535	A2	20000309	WO 1999-US19663	19990901
WO 2000012535	A3	20000608		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE,

DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 2002018782	A1	20020214	US 1999-388089	19990831
AU 9957894	A1	20000321	AU 1999-57894	19990901
EP 1109454	A2	20010627	EP 1999-945257	19990901

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.: US 1998-98685P P 19980901
WO 1999-US19663 W 19990901

AB The invention discloses the Neisseria meningitidis NMASP protein and cDNA sequences, derivs. thereof (NMASP-derived polypeptides), and antibodies that specifically bind the NMASP protein and/or NMASP-derived polypeptides. The NMASP protein of the invention has limited similarity (36% sequence identity) to the DegP (HtrA) protein of E. coli and has not been previously identified in any N. meningitidis. Also disclosed are prophylactic or therapeutic compns., including immunogenic compns. like vaccines, comprising NMASP protein and/or a NMASP-derived polypeptide. The invention is particularly directed toward compns. for treating/preventing meningitis. The invention addnl. discloses methods of inducing an immune response to N. meningitidis and N. meningitidis NMASP protein and/or a NMASP-derived polypeptide in animals.

IT **260386-80-9P**, Protein NMASP (Neisseria meningitidis)
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; protein and cDNA sequences encoding Neisseria meningitidis NMASP protein, and uses thereof in treating and diagnosing meningitis)

L2 ANSWER 17 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:15224 HCAPLUS
DOCUMENT NUMBER: 132:74540
TITLE: Protein and cDNA sequences of human tumor suppressor proteins encoded by AZ-1 and AZ-2 genes, and uses thereof in the diagnosis, prevention, and/or treatment of breast cancer
INVENTOR(S): Chen, Huei Mei; Bissell, Mina
PATENT ASSIGNEE(S): USA
SOURCE: PCT Int. Appl., 120 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000000503	A1	20000106	WO 1999-US14482	19990625

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,

CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9948347 A1 20000117 AU 1999-48347 19990625
PRIORITY APPLN. INFO.: US 1998-90747P P 19980626
WO 1999-US14482 W 19990625

AB The invention provides protein and cDNA sequences of human tumor suppressor proteins encoded by AZ-1 and AZ-2 genes. Preferably, the invention relates to the tumor suppressor encoded by the AZ-1 gene and to the detection of its level in breast cells as a marker of malignancy progression and/or tumorigenic reversion. Thus, the invention also relates to the diagnosis, prevention, and/or treatment of breast cancer. The invention also concerns monoclonal or polyclonal antibodies specific to AZ-1, AZ-2 encoded protein and to AZ-1, or AZ-2 encoded protein homologs.

IT **253582-33-1P**
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; protein and cDNA sequences of human tumor suppressor proteins encoded by AZ-1 and AZ-2 genes, and uses thereof in the diagnosis, prevention, and/or treatment of breast cancer)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 18 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:762121 HCAPLUS
DOCUMENT NUMBER: 131:347336
TITLE: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
AUTHOR(S): White, Owen; Eisen, Jonathan A.; Heidelberg, John F.; Hickey, Erin K.; Peterson, Jeremy D.; Dodson, Robert J.; Haft, Daniel H.; Gwinn, Michelle L.; Nelson, William C.; Richardson, Delwood L.; Moffat, Kelly S.; Qin, Haiying; Jiang, Lingxia; Pamphile, Wanda; Crosby, Marie; Shen, Mian; Vamathevan, Jessica J.; Lam, Peter; McDonald, Lisa; Utterback, Terry; Zalewski, Celeste; Makarova, Kira S.; Aravind, L.; Daly, Michael J.; Minton, Kenneth W.; Fleischmann, Robert D.; Ketchum, Karen A.; Nelson, Karen E.; Salzberg, Steven; Smith, Hamilton O.; Venter, J. Craig; Fraser, Claire M.
CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA
SOURCE: Science (Washington, D. C.) (1999), 286(5444), 1571-1577
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The complete genome sequence of the radiation-resistant bacterium Deinococcus radiodurans R1 is composed of two chromosomes (2,648,638 and 412,348 base pairs), a megaplasmid (177,466 base pairs), and a small plasmid (45,704 base pairs), yielding a total genome of

3,284,156 base pairs. Multiple components distributed on the chromosomes and megaplasmid that contribute to the ability of D. radiodurans to survive under conditions of starvation, oxidative stress, and high amts. of DNA damage were identified. Deinococcus radiodurans represents an organism in which all systems for DNA repair, DNA damage export, desiccation and starvation recovery, and genetic redundancy are present in one cell.

IT **250313-43-0**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of the radioresistant bacterium Deinococcus radiodurans R1)

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 19 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:444338 HCAPLUS
DOCUMENT NUMBER: 131:253834
TITLE: The Cloning and Developmental Expression of Unconventional Myosin IXA (MYO9A) a Gene in the Bardet-Biedl Syndrome (BBS4) Region at Chromosome 15q22-q23
AUTHOR(S): Gorman, Susan W.; Haider, Neena B.; Grieshammer, Uta; Swiderski, Ruth E.; Kim, Esther; Welch, Juliet W.; Searby, Charles; Leng, Song; Carmi, Rivka; Sheffield, Val C.; Duhl, David M.
CORPORATE SOURCE: Chiron Corporation, Emeryville, CA, 94608, USA
SOURCE: Genomics (1999), 59(2), 150-160
CODEN: GNMCEP; ISSN: 0888-7543
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Bardet-Biedl Syndrome (BBS) is a heterogeneous, autosomal recessive disorder characterized by mental retardation, obesity, retinitis pigmentosa, syndactyly and/or polydactyly, short stature, and hypogenitalism and is caused by mutations at a no. of distinct loci. Using a positional cloning approach for identifying the BBS4 (chromosome 15) gene, we identified and cloned an unconventional myosin gene, myosin IXA (HGMW-approved symbol MYO9A). Since mutations in unconventional myosins are known to cause several human diseases, and since mutations of unconventional myosin VIIa cause retinal degeneration, we evaluated myosin IXA as a candidate for BBS. We exploited PCR-based techniques to clone a 8473-nt cDNA for myosin IXA. A 7644-bp open reading frame predicts a protein with all the hallmarks of class IX unconventional myosins. Human Northern blot anal. and in situ hybridization of mouse embryos reveal that myosin IXA is expressed in many tissues consistent with BBS. Intron/exon boundaries were identified, and myosin IXA DNA and RNA from BBS4 patients were evaluated for mutation. (c) 1999 Academic Press.

IT **244613-54-5**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; cloning, cDNA sequence, and mRNA expression of unconventional myosin IXA gene (MYO9A), a gene in the Bardet-Biedl Syndrome (BBS4) region at chromosome 15q22-q23)

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE

FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 20 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:271499 HCAPLUS
DOCUMENT NUMBER: 130:292458
TITLE: The amino acid and nucleic acid sequences of Myosin IXa and cyclic nucleotide gated channel and their uses in diagnosis and treatment of human diseases
INVENTOR(S): Gorman, Susan W.; Welch, Julie; Duhl, David; Leng, Song; Adams, Arwen; Sheffield, Val; Chiu, Choi Ying
PATENT ASSIGNEE(S): Chiron Corporation, USA
SOURCE: PCT Int. Appl., 69 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9919489	A1	19990422	WO 1998-US21971	19981014
W: AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, CZ, DE, DE, DK, DK, EE, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9910986	A1	19990503	AU 1999-10986	19981014
US 6300485	B1	20011009	US 1998-172422	19981014

PRIORITY APPLN. INFO.:

US 1997-62858P	P	19971015
US 1997-62241P	P	19971017
US 1997-68953P	P	19971230
WO 1998-US21971	W	19981014

AB The amino acid and nucleic acid sequences of a new cyclic nucleotide gated channel-15 (CNGC-15) and Myosin IXa that map to the region of the human chromosome assocd. with Bardet-Biedl Syndrome are disclosed. CNGCs comprise a family of multimeric protein ion channels that open in response to the binding of a cyclic nucleotide to an intracellular domain. The two new proteins, CNGC-15 and Myosin IXa, are useful in the study, diagnosis and treatment of Bardet-Biedl Syndrome and Usher Syndrome. Other indications that can be treated by CNGC-15 and/or Myosin IXa polypeptides, or agonists or antagonists include hearing loss, retinitis pigmentosa, obesity, hypogonadism, sterility, polydactyly, brachydactyly, syndactyly, mental retardation, renal abnormalities, hypertension, diabetes and cardiovascular abnormalities. Compns. and methods for expressing CNGC and Myosin IXa are provided. The compns. comprise CNGC-15 and Myosin IXa and polypeptides and derivs. thereof, nucleotide sequences, expression cassettes, transformed cells and antibodies to these polypeptides. Methods for the expression and detection of CNGC and Myosin IXa nucleotides and polypeptides and compns. for the treatment of these conditions are also provided.

IT **222964-43-4**, Myosin IXa (human clone BAC)
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; amino acid and nucleic acid sequences of Myosin IXa and cyclic nucleotide gated channel (CNGC) and uses in diagnosis and treatment of human diseases)
REFERENCE COUNT: 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 21 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:63638 HCAPLUS
DOCUMENT NUMBER: 130:265212
TITLE: Myr 7 is a novel myosin IX-RhoGAP expressed in rat brain
AUTHOR(S): Chieregatti, Evelina; Gartner, Annette; Stoffler, Hanns-Eugen; Bahler, Martin
CORPORATE SOURCE: Friedrich-Miescher Laboratorium in the Max-Planck Society, Tubingen, 72076, Germany
SOURCE: Journal of Cell Science (1998), 111(24), 3597-3608
CODEN: JNCSAI; ISSN: 0021-9533
PUBLISHER: Company of Biologists Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Rho family GTPases are important regulators of neuronal morphol., but the proteins directly controlling their activity in neurons are still poorly defined. The authors report the identification of myr 7, a novel unconventional myosin IX-RhoGAP expressed in rat brain. Myr 7 is a multidomain protein related to myr 5, the first class IX myosin to be characterized. It exhibits a myosin head domain with an N-terminal extension and a large insertion at loop 2, an actin contact site and regulator of myosin ATPase rate. The myosin head domain is followed by a neck domain consisting of six unevenly spaced consecutive IQ motifs representing light chain binding sites. The tail domain contains a C6H2-zinc binding motif and a region that specifically stimulates the GTPase-activity of Rho followed by a short stretch predicted to adopt a coiled-coil structure. Five alternatively spliced regions, one in the 5'-noncoding region, two in the myosin head and two in the tail domain, were noted. Anal. of myr 7 and myr 5 expression in different tissues revealed that myr 7 is expressed at high levels in developing and adult brain tissue whereas myr 5 is expressed only at moderate levels in embryonic brain tissue and at even further reduced levels in adult brain tissue. Myr 5 is, however, highly expressed in lung, liver, spleen and testis. Myr 7 is expressed in all brain regions and is localized in the cytoplasm of cell bodies, dendrites and axons. Myr 5 exhibits an overlapping, but not identical cellular distribution. Finally, a myr 7 fusion protein encompassing the GAP domain specifically activates the GTPase-activity of Rho in vitro, and overexpression of myr 7 in HtTA1-HeLa cells leads to inactivation of Rho in vivo. These results are compatible with a role for myr 7 (and myr 5) in regulating Rho activity in neurons and hence in regulating neuronal morphol. and function.
IT **221651-87-2**
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); PROC (Process)

(amino acid sequence; cDNA sequence of human and rat myr 7, a novel myosin IX-rhoGAP expressed in rat brain)
REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 22 OF 23 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:9860 HCAPLUS
DOCUMENT NUMBER: 130:77730
TITLE: sequence of human and mouse neuro-growth factor like protein Zneu1 and antibodies for detection strategies
INVENTOR(S): Sheppard, Paul O.; Jelinek, Laura J.; Whitmore, Theodore E.; Blumberg, Hal; Lehner, Joyce M.
PATENT ASSIGNEE(S): Zymogenetics, Inc., USA
SOURCE: PCT Int. Appl., 70 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9857983	A2	19981223	WO 1998-US12763	19980618
WO 9857983	A3	19990318		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9879798	A1	19990104	AU 1998-79798	19980618
AU 737132	B2	20010809		
EP 996628	A2	20000503	EP 1998-930397	19980618
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002506349	T2	20020226	JP 1999-504836	19980618

PRIORITY APPLN. INFO.:
US 1997-50143P P 19970618
US 1997-878322 A 19970618
WO 1998-US12763 W 19980618

AB A novel mammalian neuro-growth factor like polypeptide Zneu1, polynucleotides encoding the polypeptides, and related compns. and detection methods including antibodies and anti-idiotypic antibodies and humanized antibodies and antibody fragments single-chain antibodies are presented. An expression vector is described for effective Zneu1 protein expression in a eukaryotic cell. In addn., chimeric proteins involving Zneu1 are described.

IT **218778-65-5 218778-68-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence of human and mouse neuro-growth factor like protein Zneu1 and antibodies for detection strategies)

L2 ANSWER 23 OF 23 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1996:319778 HCAPLUS
DOCUMENT NUMBER: 125:82238
TITLE: Distinct cellular and subcellular patterns of expression imply distinct functions for the Drosophila homologs of moesin and the neurofibromatosis 2 tumor suppressor, merlin
AUTHOR(S): McCartney, Brooke M.; Fehon, Richard G.
CORPORATE SOURCE: Dev., Cell., Molecular Biol. Group., Dep. Zoology, Duke Univ., Durham, NC, 27708-1000, USA
SOURCE: J. Cell Biol. (1996), 133(4), 843-852
CODEN: JCLBA3; ISSN: 0021-9525
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Interest in members of the protein 4.1 super-family, which includes the ezrin-radixin-moesin (ERM) group, has been stimulated recently by the discovery that the human neurofibromatosis 2 (NF2) tumor suppressor gene encodes an ERM-like protein, merlin. Although many proteins in this family are thought to act by linking the actin-based cytoskeleton to transmembrane proteins, the cellular functions of merlin have not been defined. To investigate the cellular and developmental functions of these proteins, Drosophila homologs of moesin (Dmoesin) and the NF2 tumor suppressor merlin (Dmerlin) were identified and characterized. Specific antibodies were used to show that although these proteins are frequently coexpressed in developing tissues, they display distinct subcellular localizations. Whereas Dmoesin is obsd. in continuous assocn. with the plasma membrane, as a typical for an ERM family protein, Dmerlin is found in punctate structures at the membrane and in cytoplasm. Investigation of Dmerlin in cultured cells demonstrates that it is assocd. with endocytic compartments. As a result of these studies, the merlin protein is proposed to have unique functions in the cell which differ from those of other ERM family members.

IT **178535-96-1**
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(amino acid sequence; distinct cellular and subcellular patterns of expression imply distinct functions for the Drosophila homologs of moesin and the neurofibromatosis 2 tumor suppressor merlin)

SELECT IS APPROXIMATELY 69% COMPLETE
E1 THROUGH E28 ASSIGNED

FILE 'REGISTRY' ENTERED AT 15:41:33 ON 07 JUN 2002
L3 28 SEA FILE=REGISTRY ABB=ON PLU=ON (178535-96-1/BI OR 218778-65-5/BI OR 218778-68-8/BI OR 221651-87-2/BI OR 222964-43-4/BI OR 244613-54-5/BI OR 250313-43-0/BI OR 253582-33-1/BI OR 260386-80-9/BI OR 262988-39-6/BI OR 263525-23-1/BI OR 284706-28-1/BI OR 316927-56-7/BI OR 319502-44-8/BI OR 324745-26-8/BI OR 326928-35-2/BI OR 331287-05-9/BI OR 332001-59-9/BI OR 332001-60-2/BI OR 342874-40-2/BI OR 352374-90-4/BI OR 352374-91-5/BI OR 352374-92-6/BI OR 355157-34-5/BI OR 369659-63-2/BI OR 371995-57-2/BI OR 403520-71-8/BI OR 403546-70-3/BI)

L4 28 L3 AND L1

L4 ANSWER 1 OF 28 REGISTRY COPYRIGHT 2002 ACS

RN **403546-70-3** REGISTRY
CN Protein (human clone WO0188088-SEQID-14753 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2753: PN: WO0188088 SEQID: 14753 claimed protein
CI MAN
SQL 108

SEQ 1 SHAGCLIRFW RKSMTPTHSL PLTPTFLGTC EASFLEPRAS PVPPQCSMAL
======
51 RRYRLDMGQS FWGGLPSSHP PDPSRPGFVP GVGHVPGQEG PGGKPAPDSS
101 XHXDPTGG
HITS AT: 35-40

REFERENCE 1: 136:227947

L4 ANSWER 2 OF 28 REGISTRY COPYRIGHT 2002 ACS
RN **403520-71-8** REGISTRY
CN Protein (human clone WO0188088-SEQID-12024 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 24: PN: WO0188088 SEQID: 12024 claimed protein
CI MAN
SQL 75

SEQ 1 GHTGPLGSPW SSVWVCLAGR QVPGPQHPHR PPGCSWGCRP PAGTGPRLPS
51 ASAPRCCPPR MRLEPRASRR SGTSG
======
HITS AT: 63-68

REFERENCE 1: 136:227947

L4 ANSWER 3 OF 28 REGISTRY COPYRIGHT 2002 ACS
RN **371995-57-2** REGISTRY
CN Protein (Propionibacterium acnes strain ATCC6919 clone WO0181581-SEQID-896 open reading frame) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 896: PN: WO0181581 SEQID: 896 claimed protein
CI MAN
SQL 125

SEQ 1 RISQHVLARR GAHDRRNRCE AGLASSTPPT LTHNEFVAVV GWGHNYRLQN
51 SDRPDRLREF GQFFLVKHFT RLARVRRDLI HGDELEPRAS NTFVYRVAVS
======
101 TSVINALFVI IIEIRALKQL SETPP
HITS AT: 85-90

REFERENCE 1: 135:353807

L4 ANSWER 4 OF 28 REGISTRY COPYRIGHT 2002 ACS
RN **369659-63-2** REGISTRY
CN Protein (human clone WO0179449-SEQID-7642 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 116: PN: WO0179449 SEQID: 2145 claimed sequence
CI MAN
SQL 119

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SEQ      1 LTQLKTHCPL IKSKTMNKKR AIREPAQEPG PQKEENPKKH RSPSFTSTSF
        51 PGLEVPASYS PPTKAEQPGQ VRKAVQPAVR LEPRASHPAG PPVPPSGVLV
                                            ======

       101 SRRRPEPGQG KPPESDFDH
HITS AT:    81-86

REFERENCE   1:  135:353783

L4   ANSWER 5 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   355157-34-5  REGISTRY
CN   Protein ECTACC (human) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AF220152-derived protein GI 7934572
CI   MAN
SQL  906

SEQ      1 MFWYKRRGAP MRPVSVIDGV VCVSPGCGSE TVPVPDGPRS DSVEGSPFRP
        51 PSHSFSAVFD EDKPIASSGT YNLDFDNIEL VDTFQTLEPR ASDAKNQEGK
                                               ==== ==
       101 VNTRRKSTDS VPISKSTLSR SLSLQASDFD GASSSGNPEA VALAPDAYST
       151 GSSSASSTLK RTKKPRPPSL KKKQTTKKPT ETPPVKETQQ EPDEESLVPS
       201 GENLASETKT ESAKTEGPSP ALLEETPLEP AVGPKAACPL DSESAEGVVP
       251 PASGGGRVQN SPPVGRKTLP LTTAPEAGEV TPSDSGGQED SPAKGLSVRL
       301 EFDYSEDKSS WDNQQENPPP TKKIGKKPVA KMPLRRPKMK KTPEKLDNTP
       351 ASPPRSPAEP NDIPIAKGTY TFDIDKWDDP NFNPFSSTSK MQESPKLPQQ
       401 SYNFDPDTCD ESVDPFKTSS KTPSSPSKSP ASFEIPASAM EANGVDGDGL
       451 NKPAKKKKTP LKTDTFRVKK SPKRSPLSDP PSQDPTPAAT PETPPVISAV
       501 VHATDEEKLA VTNQKWTCMT VDLEADKQDY PQPSDLSTFV NETKFSSPTE
       551 ELDYRNSYEI EYMEKIGSSL PQDDDAPKKQ ALYLMFDTSQ ESPVKSSPVR
       601 MSESPTPCSG SSFEETEALV NTAAKNQHPV PRGLAPNQES HLQVPEKSSQ
       651 KELEAMGLGT PSEAIEIREA AHPTDVSISK TALYSRIGTA EVEKPAGLLF
       701 QQPDLDSALQ IARAEIITKE REVSEWKDKY EESRREVMEM RKIVAEYEKT
       751 IAQMIEDEQR EKSVSHQTVQ QLVLEKEQAL ADLNSVEKSL ADLFRRYEKM
       801 KEVLEGFRKN EEVLKRCAQE YLSRVKKEEQ RYQALKVHAE EKLDRANAEI
       851 AQVRGKAQQE QAAHQASLRK EQLRVDALER TLEQKNKEIE ELTKICDELI
       901 AKMGKS
HITS AT:    87-92

REFERENCE   1:  135:176236

L4   ANSWER 6 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   352374-92-6  REGISTRY
CN   Protein (human clone 784CIF2_39 precursor) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   688: PN: WO0153312 SEQID: 1825 claimed protein
CI   MAN
SQL  1025

SEQ      1 MAYASWQRWS PVEWARWMWT AVTSSGDSSL LVLQGDSGKR SSDSEEAFET
        51 PESTTPVKAP PAPPPPPPEV IPEPEVSTQP PPEEPGCGSE TVPVPDGPRS
       101 DSVEGSPFRP PSHSFSAVFD EDKPIASSGT YNLDFDNIEL VDTFQTLEPR
                                                        ====
       151 ASDAKNQEGK VNTRRKSTDS VPISKSTLSR SLSLQASDFD GASSSGNPEA
           ==
       201 VALAPDAYST GSSSASSTLK RTKKPRPPSL KKKQTTKKPT ETPPVKETQQ
       251 EPDEESLVPS GENLASETKT ESAKTEGPSP ALLEETPLEP AVGPKAACPL
       301 DSESAEGVVP PASGGGRVQN SPPVGRKTLP LTTAPEAGEV TPSDSGGQED
       351 SPAKGLSVRL EFDYSEDKSS WDNQQENPPP TKKIGKKPVA KMPLRRPKMK
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       401 KTPEKLDNTP ASPPRSPAEP NDIPIAKGTY TFDIDKWDDP NFNPFSSTSK
       451 MQESPKLPQQ SYNFDPDTCD ESVDPFKTSS KTPSSPSKSP ASFEIPASAM
       501 EANGVDGDGL NKPAKKKTP LKTMVEDVMS VCSLFDTFRV KKSPKRSPLS
       551 DPPSQDPTPA ATPETPPVIS AVVHATDEEK LAVTNQKWTC MTVDLEADKQ
       601 DYPQPSDLST FVNETKFSSP TEELDYRNSY EIEYMEKIGS SLPQDDDAPK
       651 KQALYLMFDT SQESPVKSSP VRMSESPTPC SGSSFEETEA LVNTAAKNQH
       701 PVPRGLAPNQ ESHLQVPEKS SQKELEAMGL GTPSEAIEIT APEGSFASAD
       751 ALLSRLAHPV SLCGALDYLE PDLAEKNPPL FAQKLQREAA HPTDVSISKT
       801 ALYSRIGTAE VEKPAGLLFQ QPDLDSALQI ARAEIITKER EVSEWKDKYE
       851 ESRREVMEMR KIVAEYEKTI AQMIEDEQRE KSVSHQTVQQ LVLEKEQALA
       901 DLNSVEKSLA DLFRRYEKMK EVLEGFRKNE EVLKRCAQEY LSRVKKEEQR
       951 YQALKVHAEE KLDRANAEIA QVRGKAQQEQ AAHQASLRKE QLRVDALERT
      1001 LEQKNKEIEE LTKICDELIA KMGKS
HITS AT:   147-152

REFERENCE   1:  135:148240

L4   ANSWER 7 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   352374-91-5  REGISTRY
CN   Protein (human clone 784CIF2_38 precursor) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   687: PN: WO0153312 SEQID: 1824 claimed protein
CI   MAN
SQL  966

SEQ      1 MAYASWQRWS PVEWARWMWT AVTSSGDSSL LVLQGDSGKR SSDSEEAFET
         51 PESTTPVKAP PAPPPPPPEV IPEPEVSTQP PPEEPGCGSE TVPVPDGPRS
        101 DSVEGSPFRP PSHSFSAVFD EDKPIASSGT YNLDFDNIEL VDTFQTLEPR
                                                              ====
        151 ASDAKNQEGK VNTRRKSTDS VPISKSTLSR SLSLQASDFD GASSSGNPEA
            ==
        201 VALAPDAYST GSSSASSTLK RTKKPRPPSL KKKQTTKKPT ETPPVKETQQ
        251 EPDEESLVPS GENLASETKT ESAKTEGPSP ALLEETPLEP AVGPKAACPL
        301 DSESAEGVVP PASGGGRVQN SPPVGRKTLP LTTAPEAGEV TPSDSGGQED
        351 SPAKGLSVRL EFDYSEDKSS WDNQQENPPP TKKIGKKPVA KMPLRRPKMK
        401 KTPEKLDNTP ASPPRSPAEP NDIPIAKGTY TFDIDKWDDP NFNPFSSTSK
        451 MQESPKLPQQ SYNFDPDTCD ESVDPFKTSS KTPSSPSKSP ASFEIPASAM
        501 EANGVDGDGL NKPAKKKTP LKTDTFRVKK SPKRSPLSDP PSQDPTPAAT
        551 PETPPVISAV VHATDEEKLA VTNQKWTCMT VDLEADKQDY PQPSDLSTFV
        601 NETKFSSPTE ELDYRNSYEI EYMEKIGSSL PQDDDAPKKQ ALYLMFDTSQ
        651 ESPVKSSPVR MSESPTPCSG SSFEETEALV NTAAKNQHPV PRGLAPNQES
        701 HLQVPEKSSQ KELEAMGLGT PSEAIEIREA AHPTDVSISK TALYSRIGTA
        751 EVEKPAGLLF QQPDLDSALQ IARAEIITKE REVSEWKDKY EESRREVMEM
        801 RKIVAEYEKT IAQMIEDEQR EKSVSHQTVQ QLVLEKEQAL ADLNSVEKSL
        851 ADLFRRYEKM KEVLEGFRKN EEVLKRCAQE YLSRVKKEEQ RYQALKVHAE
        901 EKLDRANAEI AQVRGKAQQE QAAHQASLRK EQLRVDALER TLEQKNKEIE
        951 ELTKICDELI AKMGKS
HITS AT:   147-152

REFERENCE   1:  135:148240

L4   ANSWER 8 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   352374-90-4  REGISTRY
CN   Protein (human clone 784CIF2_37 precursor) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   686: PN: WO0153312 SEQID: 1823 claimed protein
CI   MAN
SQL  1013
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SEQ      1 MAYASWQRWS PVEWARWMWT AVTSSGDSSL LVLQGDSGKR SSDSEEAFET
        51 PESTTPVKAP PAPPPPPPEV IPEPEVSTQP PPEEPGCGSE TVPVPDGPRS
       101 DSVEGSPFRP PSHSFSAVFD EDKPIASSGT YNLDFDNIEL VDTFQTLEPR
                                                          ====
       151 ASDAKNQEGK VNTRRKSTDS VPISKSTLSR SLSLQASDFD GASSSGNPEA
           ==
       201 VALAPDAYST GSSSASSTLK RTKKPRPPSL KKKQTTKKPT ETPPVKETQQ
       251 EPDEESLVPS GENLASETKT ESAKTEGPSP ALLEETPLEP AVGPKAACPL
       301 DSESAEGVVP PASGGGRVQN SPPVGRKTLP LTTAPEAGEV TPSDSGGQED
       351 SPAKGLSVRL EFDYSEDKSS WDNQQENPPP TKKIGKKPVA KMPLRRPKMK
       401 KTPEKLDNTP ASPPRSPAEP NDIPIAKGTY TFDIDKWDDP NFNPFSSTSK
       451 MQESPKLPQQ SYNFDPDTCD ESVDPFKTSS KTPSSPSKSP ASFEIPASAM
       501 EANGVDGDGL NKPAKKKKTP LKTDTFRVKK SPKRSPLSDP PSQDPTPAAT
       551 PETPPVISAV VHATDEEKLA VTNQKWTCMT VDLEADKQDY PQPSDLSTFV
       601 NETKFSSPTE ELDYRNSYEI EYMEKIGSSL PQDDDAPKKQ ALYLMFDTSQ
       651 ESPVKSSPVR MSESPTPCSG SSFEETEALV NTAAKNQHPV PRGLAPNQES
       701 HLQVPEKSSQ KELEAMGLGT PSEAIEITAP EGSFASADAL LSRLAHPVSL
       751 CGALDYLEPD LAEKNPPLFA QKLQREAAHP TDVSISKTAL YSRIGTAEVE
       801 KPAGLLFQQP DLDSALQIAR AEIITKEREV SEWKDKYEES RREVMEMRKI
       851 VAEYEKTIAQ MIEDEQREKS VSHQTVQQLV LEKEQALADL NSVEKSLADL
       901 FRRYEKMKEV LEGFRKNEEV LKRCAQEYLS RVKKEEQRYQ ALKVHAEEKL
       951 DRANAEIAQV RGKAQQEQAA HQASLRKEQL RVDALERTLE QKNKEIEELT
      1001 KICDELIAKM GKS
HITS AT:    147-152

REFERENCE   1:  135:148240

L4    ANSWER 9 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN    342874-40-2  REGISTRY
CN    Calcium channel (Rattus norvegicus brain subunit .alpha.1H) (9CI)
      (CA INDEX NAME)
OTHER NAMES:
CN    Calcium channel (rat brain subunit .alpha.1H)
CN    GenBank AF290213-derived protein GI 11415018
CI    MAN
SQL   2359

SEQ      1 MTEGTLAADE VRVPLGASPP APAAPVRASP ASPGAPGREE QGGSGSGVLA
        51 PESPGTECGA DLGADEEQPV PYPALAATVF FCLGQTTRPR SWCLRLVCNP
       101 WFEHVSMLVI MLNCVTLGMF RPCEDVECRS ERCSILEAFD DFIFAFFAVE
       151 MVIKMVALGL FGQKCYLGDT WNRLDFFIVM AGMMEYSLDG HNVSLSAIRT
       201 VRVLRPLRAI NRVPSMRILV TLLLDTLPML GNVLLLCFFV FFIFGIVGVQ
       251 LWAGLLRNRC FLDSAFVRNN NLTFLRPYYQ TEEGEENPFI CSSRRDNGMQ
       301 KCSHIPSRRE LRVQCTLGWE AYGQPQAEDG GAGRNACINW NQYYNVCRSG
       351 EFNPHNGAIN FDNIGYAWIA IFQVITLEGW VDIMYYVMDA HSFYNFIYFI
       401 LLIIMGSFFM INLCLVVIAT QFSETKQREN QLMREQRARY LSNDSTLASF
       451 SEPGSCYEEL LKYVGHIFRK VKRRSLRLYA RWQSRWRKKV DPSSTVHGQG
       501 PGRRPRRAGR RTASVHHLVY HHHHHHHHHY HFSHGGPRRP SPEPGAGDNR
       551 LVRACAPPSP PSPGHGPPDS ESVHSIYHAD CHVEGPQERA RVAHSIATAA
       601 SLKLASGLGT MNYPTILPSG TVNSKGGTSS RPKGLRGAGA PGAAVHSPLS
       651 LGSPRPYEKI QDVVGEQGLG RASSHLSGLS VPCPLPSPQA GTLTCELKSC
       701 PYCASALEDP EFEFSGSESG DSDAHGVYEF TQDVRHGDCR DPVQQPHEVG
       751 TPGHSNERRR TPLRKASQPG GIGHLWASFS GKLRRIVDSK YFNRGIMAAI
       801 LVNTLSMGVE YHEQPEELTN ALEISNIVFT SMFALEMLLK LLACGPLGYI
       851 RNPYNIFDGI VVVISVWEIV GQADGGQSVL RTFRLLRVLK LVRFLPALRR
       901 QLVVLMRTMD NVATFCMLLM LFIFIFSILG MHLFGCKFSL KTDSGDTVPD
       951 RKNFDSLLWA IVTVFQILTQ EDWNVVLYNG MASTSSWAAL YFVALMTFGN
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      1001 YVLFNLLVAI LVEGFQAEGD ATRSDTDEDK TSTQLEGDFD KLRDLRATEM
      1051 KMYSLAVTPN GHLEGRGSLP PPLITHTAAT PMPTPKSSPN LDVAHALLDS
      1101 RRSSSGSVDP QLGDQKSLAS LRSSPCTPWG PNSAGSSRRS SWNSLGRAPS
      1151 LKRRNQCGER ESLLSGEGKG STDDEAEDSR PSTGTHPGAS PGPRATPLRR
      1201 AESLDHRSTL DLCPPRPAAL LPTKFHDCNG QMVALPSEFF LRIDSHKEDA
      1251 AEFDDDIEDS CCFRLHKVLE PYAPQWCRSR ESWALYLFPP QNRLRVSCQK
      1301 VIAHKMFDHV VLVFIFLNCI TIALERPDID PGSTERAFLS VSNYIFTAIF
      1351 VVEMMVKVVA LGLLWGEHAY LQSSWNVLDG LLVLVSLVDI IVAMASAGGA
      1401 KILGVLRVVR LLRTLRPLRV ISRAPGLKLV VETLISSLRP IGNIVLICCA
      1451 FFIIFGILGV QLFKGKFYYC EGTDTRNITT KAECHAAHYR WVRRKYNFDN
      1501 LGQALMSLFV LSSKDGWVNI MYDGLDAVGI DQQPVQNHNP WMLLYFISFL
      1551 LIVSFFVLNM FVGVVVENFH KCRQHQEAEE ARRREEKRLR RLERRRRKAQ
      1601 RRPYYADYSH TRRSIHSLCT SHYLDLFITF IICLNVITMS MEHYNQPKSL
      1651 DEALKYCNYV FTIVFVFEAA LKLVAFGFRR FFKDRWNQLD LAIVLLSIMG
      1701 IALEEIEMNA ALPINPTIIR IMRVLRIARV LKLLKMATGM RALLDTVVQA
      1751 LPQVGNLGLL FMLLFFIYAA LGVELFGRLE CSEDNPCEGL SRHATFTNFG
      1801 MAFLTLFRVS TGDNWNGIMK DTLRECTRED KHCLSYLPAL SPVYFVTFML
      1851 VAQFVLVNVV VAVLMKHLEE SNKEAREDAE MDAEIELEMA QGSTAQPPPT
      1901 AQESQGTQPD TPNLLVVRKV SVSRMLSLPN DSYMFRPVAP AAAPHSHPLQ
      1951 EVEMETYTGP VTSAHSPPLE PRASFQVPSA ASSPARVSDP LCALSPRGTP
                               == ====
      2001 RSLSLSRILC RQEAMHSESL EGKVDDVGGD SIPDYTEPAE NMSTSQASTG
      2051 APRSPPCSPR PASVRTRKHT FGQRCISSRP PTLGGDEAEA ADPADEEVSH
      2101 ITSSAHPWPA TEPHSPEASP TASPVKGTMG SGRDPRRFCS VDAQSFLDKP
      2151 GRPDAQRWSS VELDNGESHL ESGEVRGRAS ELEPALGSRR KKKMSPPCIS
      2201 IEPPTKDEGS SRPPAAEGGN TTLRRRTPSC EAALHRDCPE PTEGPGTGGD
      2251 PVAKGERWGQ ASCRAEHLTV PNFAFEPLDM GGPGGDCFLD SDQSVTPEPR
      2301 VSSLGAIVPL ILETELSMPS PDCPEKEQGL YLTVPQTPLK KPGSTPATPA
      2351 PDDSGDEPV
HITS AT:    1969-1974

REFERENCE   1:  135:15597

L4    ANSWER 10 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN    332001-60-2  REGISTRY
CN    Bone morphogenetic protein receptors, protein BRK-3 (mouse clone
      pJT6-mBRK-3L) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN    7: PN: US6210899 SEQID: 8 claimed protein
CI    MAN
SQL   2887

SEQ       1 METTHRSERS ERLEHISARG PRPHEARGVA LPRTRPLELE TRPALAVALL
         51 ELEVALSERT HRTHRALAAL ASERGLNASN GLNGLARGLE CYSALAPHEL
        101 YSASPPRTYR GLNGLNASPL EGLYILEGLY GLSERARGIL ESERHISGLA
        151 SNGLYTHRIL ELECYSSERL YSGLYSERTH RCYSTYRGLY LETRPGLLYS
        201 SERLYSGLYA SPILEASNLE VALLYSGLNG LYCYSTRPSE RHISILEGLY
        251 ASPPRGLNGL CYSHISTYRG LGLCYSVALV ALTHRTHRTH RPRPRSERIL
        301 EGLNASNGLY THRTYRARGP HECYSCYSCY SSERTHRASP LECYSASNVA
        351 LASNPHETHR GLASNPHEPR PRPRASPTHR THRPRLESER PRPRHISSER
        401 PHEASNARGA SPGLTHRILE ILEILEALAL EALASERVAL SERVALLEAL
        451 AVALLEILEV ALALALECYS PHEGLYTYRA RGMETLETHR GLYASPARGL
        501 YSGLNGLYLE HISSERMETA SNMETMETGL ALAALAALAA LAGLPRSERL
        551 EASPLEASPA SNLELYSLEL EGLLEILEGL YARGGLYARG TYRGLYALAV
        601 ALTYRLYSGL YSERLEASPG LARGPRVALA LAVALLYSVA LPHESERPHE
        651 ALAASNARGG LNASNPHEIL EASNGLLYSA SNILETYRAR GVALPRLEME
        701 TGLHISASPA SNILEALAAR GPHEILEVAL GLYASPGLAR GLETHRALAA
        751 SPGLYARGME TGLTYRLELE VALMETGLTY RTYRPRASNG LYSERLECYS
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       801 LYSTYRLESE RLEHISTHRS ERASPTRPVA LSERSERCYS ARGLEALAHI
       851 SSERVALTHR ARGGLYLEAL ATYRLEHIST HRGLLEPRAR GGLYASPHIS
       901 TYRLYSPRAL AILESERHIS ARGASPLEAS NSERARGASN VALLEVALLY
       951 SASNASPGLY ALACYSVALI LESERASPPH EGLYLESERM ETARGLETHR
      1001 GLYASNARGL EVALARGPRG LYGLGLASPA SNALAALAIL ESERGLVALG
      1051 LYTHRILEAR GTYRMETALA PRGLVALLEG LGLYALAVAL ASNLEARGAS
      1101 PCYSGLSERA LALELYSGLN VALASPMETT YRALALEGLY LEILETYRTR
      1151 PGLVALPHEM ETARGCYSTH RASPLEPHEP RGLYGLSERV ALPRASPTYR
      1201 GLNMETALAP HEGLNTHRGL VALGLYASNH ISPRTHRPHE GLASPMETGL
      1251 NVALLEVALS ERARGGLLYS GLNARGPRLY SPHEPRGLAL ATRPLYSGLA
      1301 SNSERLEALA VALARGSERL ELYSGLTHRI LEGLASPCYS TRPASPGLNA
      1351 SPALAGLALA ARGLETHRAL AGLNCYSALA GLGLARGMET ALAGLLEMET
      1401 METILETRPG LARGASNLYS SERVALSERP RTHRVALASN PRMETSERTH
      1451 RALAMETGLN ASNGLARGAS NLESERHISA SNARGARGVA LPRLYSILEG
      1501 LYPRTYRPRA SPTYRSERSE RSERSERTYR ILEGLASPSE RILEHISHIS
      1551 THRASPSERI LEVALLYSAS NILESERSER GLHISSERME TSERSERTHR
      1601 PRLETHRILE GLYGLLYSAS NARGASNSER ILEASNTYRG LARGGLNGLN
      1651 ALAGLNALAA RGILEPRSER PRGLTHRSER VALTHRSERL ESERTHRASN
      1701 THRTHRTHRT HRASNTHRTH RGLYLETHRP RSERTHRGLY METTHRTHRI
      1751 LESERGLMET PRTYRPRASP GLTHRHISLE HISALATHRA SNVALALAGL
      1801 NSERILEGLY PRTHRPRVAL CYSLEGLNLE THRGLGLASP LEGLTHRASN
      1851 LYSLEASPPR LYSGLVALAS PLYSASNLEL YSGLSERSER ASPGLASNLE
      1901 METGLHISSE RLELYSGLNP HESERGLYPR ASPPRLESER SERTHRSERS
      1951 ERSERLELET YRPRLEILEL YSLEALAVAL GLVALTHRGL YGLNGLNASP
      2001 PHETHRGLNA LAALAASNGL YGLNALACYS LEILEPRASP VALPRPRALA
                                             ======
      2051 GLNILETYRP RLEPRLYSGL NGLNASNLEP RLYSARGPRT HRSERLEPRL
      2101 EASNTHRLYS ASNSERTHRL YSGLPRARGL ELYSPHEGLY ASNLYSHISL
      2151 YSSERASNLE LYSGLNVALG LTHRGLYVAL ALALYSMETA SNTHRILEAS
      2201 NALAALAGLP RHISVALVAL THRVALTHRM ETASNGLYVA LALAGLYARG
      2251 SERHISASNV ALASNSERHI SALAALATHR THRGLNTYRA LAASNGLYAL
      2301 AVALPRALAG LYGLNALAAL AASNILEVAL ALAHISARGS ERGLNGLMET
      2351 LEGLNASNGL NPHEILEGLY GLASPTHRAR GLEASNILEA SNSERSERPR
      2401 ASPGLHISGL PRLELEARGA RGGLGLNGLN ALAGLYHISA SPGLGLYVAL
      2451 LEASPARGLE VALASPARGA RGGLARGPRL EGLGLYGLYA RGTHRASNSE
      2501 RASNASNASN ASNSERASNP RCYSSERGLG LNASPILELE THRGLNGLYV
      2551 ALTHRSERTH RALAALAASP PRGLYPRSER LYSPRARGAR GALAGLNARG
      2601 PRASNSERLE ASPLESERAL ATHRASNILE LEASPGLYSE RSERILEGLN
      2651 ILEGLYGLSE RTHRGLNASP GLYLYSSERG LYSERGLYGL LYSILELYSA
      2701 RGARGVALLY STHRPRTYRS ERLELYSARG TRPARGPRSE RTHRTRPVAL
      2751 ILESERTHRG LPRLEASPCY SGLVALASNA SNASNGLYSE RASPARGALA
      2801 VALHISSERL YSSERSERTH RALAVALTYR LEALAGLGLY GLYTHRALAT
      2851 HRTHRTHRVA LSERLYSASP ILEGLYMETA SNCYSLE
HITS AT:    2034-2039

REFERENCE   1:  134:261275

L4    ANSWER 11 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN    332001-59-9  REGISTRY
CN    Bone morphogenetic protein receptors, protein BRK-3 (human foreskin
      fibroblast clone pHSK1040) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN    2: PN: US6210899 SEQID: 2 claimed protein
CI    MAN
SQL   2887

SEQ       1 METTHRSERS ERLEGLNARG PRTRPARGVA LPRTRPLEPR TRPTHRILEL
         51 ELEVALSERT HRALAALAAL ASERGLNASN GLNGLARGLE CYSALAPHEL
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     101 YSASPPRTYR GLNGLNASPL EGLYILEGLY GLSERARGIL ESERHISGLA
     151 SNGLYTHRIL ELECYSSERL YSGLYSERTH RCYSTYRGLY LETRPGLLYS
     201 SERLYSGLYA SPILEASNLE VALLYSGLNG LYCYSTRPSE RHISILEGLY
     251 ASPPRGLNGL CYSHISTYRG LGLCYSVALV ALTHRTHRTH RPRPRSERIL
     301 EGLNASNGLY THRTYRARGP HECYSCYSCY SSERTHRASP LECYSASNVA
     351 LASNPHETHR GLASNPHEPR PRPRASPTHR THRPRLESER PRPRHISSER
     401 PHEASNARGA SPGLTHRILE ILEILEALAL EALASERVAL SERVALLEAL
     451 AVALLEILEV ALALALECYS PHEGLYTYRA RGMETLETHR GLYASPARGL
     501 YSGLNGLYLE HISSERMETA SNMETMETGL ALAALAALAS ERGLPRSERL
     551 EASPLEASPA SNLELYSLEL EGLLEILEGL YARGGLYARG TYRGLYALAV
     601 ALTYRLYSGL YSERLEASPG LARGPRVALA LAVALLYSVA LPHESERPHE
     651 ALAASNARGG LNASNPHEIL EASNGLLYSA SNILETYRAR GVALPRLEME
     701 TGLHISASPA SNILEALAAR GPHEILEVAL GLYASPGLAR GVALTHRALA
     751 ASPGLYARGM ETGLTYRLEL EVALMETGLT YRTYRPRASN GLYSERLECY
     801 SLYSTYRLES ERLEHISTHR SERASPTRPV ALSERSERCY SARGLEALAH
     851 ISSERVALTH RARGGLYLEA LATYRLEHIS THRGLLEPRA RGGLYASPHI
     901 STYRLYSPRA LAILESERHI SARGASPLEA SNSERARGAS NVALLEVALL
     951 YSASNASPGL YTHRCYSVAL ILESERASPP HEGLYLESER METARGLETH
    1001 RGLYASNARG LEVALARGPR GLYGLGLASP ASNALAALAI LESERGLVAL
    1051 GLYTHRILEA RGTYRMETAL APRGLVALLE GLGLYALAVA LASNLEARGA
    1101 SPCYSGLSER ALALELYSGL NVALASPMET TYRALALEGL YLEILETYRT
    1151 RPGLILEPHE METARGCYST HRASPLEPHE PRGLYGLSER VALPRGLTYR
    1201 GLNMETALAP HEGLNTHRGL VALGLYASNH ISPRTHRPHE GLASPMETGL
    1251 NVALLEVALS ERARGGLLYS GLNARGPRLY SPHEPRGLAL ATRPLYSGLA
    1301 SNSERLEALA VALARGSERL ELYSGLTHRI LEGLASPCYS TRPASPGLNA
    1351 SPALAGLALA ARGLETHRAL AGLNCYSALA GLGLARGMET ALAGLLEMET
    1401 METILETRPG LARGASNLYS SERVALSERP RTHRVALASN PRMETSERTH
    1451 RALAMETGLN ASNGLARGAS NLESERHISA SNARGARGVA LPRLYSILEG
    1501 LYPRTYRPRA SPTYRSERSE RSERSERTYR ILEGLASPSE RILEHISHIS
    1551 THRASPSERI LEVALLYSAS NILESERSER GLHISSERME TSERSERTHR
    1601 PRLETHRILE GLYGLLYSAS NARGASNSER ILEASNTYRG LARGGLNGLN
    1651 ALAGLNALAA RGILEPRSER PRGLTHRSER VALTHRSERL ESERTHRASN
    1701 THRTHRTHRT HRASNTHRTH RGLYLETHRP RSERTHRGLY METTHRTHRI
    1751 LESERGLMET PRTYRPRASP GLTHRASNLE HISTHRTHRA SNVALALAGL
    1801 NSERILEGLY PRTHRPRVAL CYSLEGLNLE THRGLGLASP LEGLTHRASN
    1851 LYSLEASPPR LYSGLVALAS PLYSASNLEL YSGLSERSER ASPGLASNLE
    1901 METGLHISSE RLELYSGLNP HESERGLYPR ASPPRLESER SERTHRSERS
    1951 ERSERLELET YRPRLEILEL YSLEALAVAL GLALATHRGL YGLNGLNASP
    2001 PHETHRGLNT HRALAASNGL YGLNALACYS LEILEPRASP VALLEPRTHR
                                          ======
    2051 GLNILETYRP RLEPRLYSGL NGLNASNLEP RLYSARGPRT HRSERLEPRL
    2101 EASNTHRLYS ASNSERTHRL YSGLPRARGL ELYSPHEGLY SERLYSHISL
    2151 YSSERASNLE LYSGLNVALG LTHRGLYVAL ALALYSMETA SNTHRILEAS
    2201 NALAALAGLP RHISVALVAL THRVALTHRM ETASNGLYVA LALAGLYARG
    2251 ASNHISSERV ALASNSERHI SALAALATHR THRGLNTYRA LAASNGLYTH
    2301 RVALLESERG LYGLNTHRTH RASNILEVAL THRHISARGA LAGLNGLMET
    2351 LEGLNASNGL NPHEILEGLY GLASPTHRAR GLEASNILEA SNSERSERPR
    2401 ASPGLHISGL PRLELEARGA RGGLGLNGLN ALAGLYHISA SPGLGLYVAL
    2451 LEASPARGLE VALASPARGA RGGLARGPRL EGLGLYGLYA RGTHRASNSE
    2501 RASNASNASN ASNSERASNP RCYSSERGLG LNASPVALLE ALAGLNGLYV
    2551 ALPRSERTHR ALAALAASPP RGLYPRSERL YSPRARGARG ALAGLNARGP
    2601 RASNSERLEA SPLESERALA THRASNVALL EASPGLYSER SERILEGLNI
    2651 LEGLYGLSER THRGLNASPG LYLYSSERGL YSERGLYGLL YSILELYSLY
    2701 SARGVALLYS THRPRTYRSE RLELYSARGT RPARGPRSER THRTRPVALI
    2751 LESERTHRGL SERLEASPCY SGLVALASNA SNASNGLYSE RASNARGALA
    2801 VALHISSERL YSSERSERTH RALAVALTYR LEALAGLGLY GLYTHRALAT
    2851 HRTHRMETVA LSERLYSASP ILEGLYMETA SNCYSLE
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HITS AT: 2034-2039

Searcher : Shears 308-4994

REFERENCE 1: 134:261275

L4 ANSWER 12 OF 28 REGISTRY COPYRIGHT 2002 ACS
RN **331287-05-9** REGISTRY
CN 1: PN: WO0119971 SEQID: 1 unclaimed protein (9CI) (CA INDEX NAME)
CI MAN
SQL 682

SEQ
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      1 METSERLYSL ESERVALPHE PHEILEPHEL EPHECYSSER ILEALATHRA
     51 LAALAGLSER LEPRASPLEL YSILEGLLYS LEASPGLGLY VALTYRVALH
                  ======
    101 ISTHRSERPH EGLGLVALAS NGLYTRPGLY VALVALPRLY SHISGLYLEV
    151 ALVALLEVAL ASNALAGLAL ATYRLEILEA SPTHRPRPHE THRALALYSA
    201 SPTHRGLLYS LEVALTHRTR PPHEVALGLA RGGLYTYRLY SILELYSGLY
    251 SERILESERS ERHISPHEHI SSERASPSER THRGLYGLYI LEGLTRPLEA
    301 SNSERARGSE RILEPRTHRT YRALASERGL LETHRASNGL LELELYSLYS
    351 ASPGLYLYSV ALGLNALATH RASNSERPHE SERGLYVALA SNTYRTRPLE
    401 VALLYSASNL YSILEGLVAL PHETYRPRGL YPRGLYHIST HRPRASPASN
    451 VALVALVALT RPLEPRGLAR GLYSILELEP HEGLYGLYCY SPHEILELYS
    501 PRTYRGLYLE GLYASNLEGL YASPALAASN ILEGLALATR PPRLYSSERA
    551 LALYSLELEL YSSERLYSTY RGLYLYSALA LYSLEVALVA LPRSERHISS
    601 ERGLVALGLY ASPALASERL ELELYSLETH RLEGLGLNAL AVALLYSGLY
    651 LEASNGLSER LYSLYSPRSE RLYSPRSERA SN
```
HITS AT: 61-66

REFERENCE 1: 134:248841

L4 ANSWER 13 OF 28 REGISTRY COPYRIGHT 2002 ACS
RN **326928-35-2** REGISTRY
CN Protein (human clone PLACE1004777) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 168: PN: EP1074617 SEQID: 12736 claimed protein
CI MAN
SQL 526

SEQ
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      1 MDRASVCKLC KYACHKKCCL KTTAKCSKKY DPELSSRQFG VELSRLTSED
     51 RTVPLVVEKL INYIEMHGLY TEGIYRKSGS TNKIKELRQG LDTDAESVNL
    101 DDYNIHVIAS VFKQWLRDLP NPLMTFELYE EFLRAMGLQE RKETIRGVYS
    151 VIDQLSRTHL NTLERLIFHL VRIALQEDTN RMSANALAIV FAPCILRCPD
    201 TTDPLQSVQD ISKTTTCVEL IVVEQMNKYK ARLKDISSLE FAENKAKTRL
    251 SLIRRSMGKG RIRRGNYPGP SSPVVVRLPS VSDVSEETLT SEAAMETDIT
    301 EQQQAAMQQE ERVLTEQIEN LQKEKEELTF EMLVLEPRAS DDETLESEAS
                                        ======
    351 IGTADSSENL NMESEYAISE KSERSLALSS LKTAGKSEPS SKLRKQLKKQ
    401 QDSLDVVDSS VSSLCLSNTA SSHGTRKLFQ IYSKSPFYRA ASGNEALGME
    451 GPLGQTKFLE DKPQFISRGT FNPEKGKQKL KNVKNSPQKT KETPEGTVMS
    501 GRRKTVDPDC TSNQQLALFG NNEFMV
```
HITS AT: 335-340

REFERENCE 1: 134:188985

L4 ANSWER 14 OF 28 REGISTRY COPYRIGHT 2002 ACS
RN **324745-26-8** REGISTRY
CN L-Serine, L-leucyl-L-.alpha.-glutamyl-L-prolyl-L-arginyl-L-alanyl-
(9CI) (CA INDEX NAME)
SQL 6

SEQ 1 LEPRAS
======
HITS AT: 1-6

REFERENCE 1: 134:159864

L4 ANSWER 15 OF 28 REGISTRY COPYRIGHT 2002 ACS
RN **319502-44-8** REGISTRY
CN 8: PN: WO0102561 SEQID: 26 unclaimed protein (9CI) (CA INDEX NAME)
CI MAN
SQL 2359

SEQ
```
      1 MTEGTLAADE VRVPLGASPP APAAPVRASP ASPGAPGREE QGGSGSGVLA
     51 PESPGTECGA DLGADEEQPV PYPALAATVF FCLGQTTRPR SWCLRLVCNP
    101 WFEHVSMLVI MLNCVTLGMF RPCEDVECRS ERCSILEAFD DFIFAFFAVE
    151 MVIKMVALGL FGQKCYLGDT WNRLDFFIVM AGMMEYSLDG HKVSLSAIRT
    201 VRVLRPLRAI NRVPSMRILV TLLLDTLPML GNVLLLCFFV FFIFGIVGVQ
    251 LWAGLLRNRC FLDSAFVRNN NLTFLRPYYQ TEEGEENPFI CSSRRDNGMQ
    301 KCSHIPSRRE LRVQCTLGWE AYGQPQAEDG GAGRNACINW NQYYNVCRSG
    351 EFNPHNGAIN FDNIGYAWIA IFQVITLEGW VDIMYYVMDA HSFYNFIYFI
    401 LLIIMGSFFM INLCLVVIAT QFSETKQREN QLMREQRARY LSNDSTLASF
    451 SEPGSCYEEL LKYVGHIFRK VKRRSLRLYA RWQSRWRKKV DPSSTVHGQG
    501 PGRRPRRAGR RTASVHHLVY HHHHHHHHHY HFSHGGPRRP SPEPGAGDNR
    551 LVRACAPPSP PSPGHGPPDS ESVHSIYHAD CHVEGPQERA RVAHSIATAA
    601 SLKLASGLGT MNYPTILPSG TVNSKGGTSS RPKGLRGAGA PGAAVHSPLS
    651 LGSPRPYEKI QDVVGEQGLG RASSHLSGLS VPCPLPSPQA GTLTCELKSC
    701 PYCASALEDP EFEFSGSESG DSDAHGVYEF TQDVRHGDCR DPVQQPHEVG
    751 TPGHSNERRR TPLRKASQPG GIGHLWASFS GKLRRIVDSK YFNRGIMAAI
    801 LVNTLSMGVE YHEQPEELTN ALEISNIVFT SMFALEMLLK LLACGPLGYI
    851 RNPYNIFDGI VVVISVWEIV GQADGGQSVL RTFRLLRVLK LVRFLPALRR
    901 QLVVLMRTMD NVATFCMLLM LFIFIFSILG MHLFGCKFSL KTDSGDTVPD
    951 RKNFDSLLWA IVTVFQILTQ EDWNVVLYNG MASTSSWAAL YFVALMTFGN
   1001 YVLFNLLVAI LVEGFQAEGD ATRSDTDEDK TSTQLEGDFD KLRDLRATEM
   1051 KMYSLAVTPN GHLEGRGSLP PPLITHTAAT PMPTPKSSPN LDVAHALLDS
   1101 RRSSSGSVDP QLGDQKSLAS LRSSPCTPWG PNSAGSSRRS SWNSLGRAPS
   1151 LKRRSQCGER ESLLSGEGKG STDDEAEDSR PSTGTHPGAS PGPRATPLRR
   1201 AESLDHRSTL DLCPPRPAPP AVQVHDCNGQ MVALPSEFFL RIDSHKEDAA
   1251 EFDDDIEDSC CFRLHKVLEP YAPQWCRSRE SWALYLFPPQ NRLRVSCQKV
   1301 IAHKMFDHVV LVFIFLNCIT IALERPDIDP GSTERAFLSV SNYIFTAIFV
   1351 VEMMVKVVAL GLLWGEHAYL QSSWNVLDGL LVLVSLVDII VAMASAGGAK
   1401 ILGVLRVVRL LRTLRPLRVI SRAPGLKLVV ETLISSLRPI GNIVLICCAF
   1451 FIIFGILGVQ LFKGKFYYCE GTDTRNITTK AECHAAHYRW VRRKYNFDNL
   1501 GQALMSLFVL SSKDGWVNIM YDGLDAVGID QQPVQNHNPW MLLYFISFLL
   1551 IVSFFVLNMF VGVVVENFHK CRQHQEAEEA RRREEKRLRR LERRRRKAQR
   1601 RPYYADYSHT RRSIHSLCTS HYLDLFITFI ICLNVITMSM EHYNQPKSLD
   1651 EALKYCNYVF TIVFVFEAAL KLVAFGFRRF FKDRWNQLDL AIVLLSIMGI
   1701 ALEEIEMNAA LPINPTIIRI MRVLRIARVL KLLKMATGMR ALLDTVVQAL
   1751 PQVGNLGLLF MLLFFIYAAL GVELFGRLEC SEDNPCEGLS RHATFTNFGM
   1801 AFLTLFRVST GDNWNGIMKD TLRECTREDK HCLSYLPALS PVYFVTFMLV
   1851 AQFVLVNVVV AVLMKHLEES NKEAREDAEM DAEIELEMAQ GSTAQPPPTA
   1901 QESQGTQPDT PNLLVVRKVS VSRMLSLPND SYMFRPVAPA AAPHSHPLQE
   1951 VEMETYTGPV TSAHSPPLEP RASFQVPSAA SSPARVSDPL CALSPRGTPR
                          === ===
   2001 SLSLSRILCR QEAMHSESLE GKVDDVGGDS IPDYTEPAEN MSTSQASTGA
   2051 PRSPPCSPRP ASVRTRKHTF GQRCISSRPP TLGGDEAEAA DPADEEVSHI
   2101 TSSAHPWPAT EPHSPEASPT ASPVKGTMGS GRDPRRFCSV DAQSFLDKPG
   2151 RPDAQRWSSV ELDNGESHLE SGEVRGRASE LEPALGSRRK KKMSPPCISI
   2201 EPPTKDEGSS RPPAAEGGNT TLRRRTPSCE AALHRDCPEP TEGPGTGGDP
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      2251 VAKGERWGQA SCRAEHLTVP NFAFEPLDMG GPGGDCFLDS DQSVTPEPRV
      2301 SSLGAIVPLI LETELSMPSP DCPEKEQGLY LTVPQTPLKK PGSTPATPAP
      2351 DDSGDEPVZ
HITS AT:   1968-1973

REFERENCE   1:  134:111253

L4   ANSWER 16 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   316927-56-7  REGISTRY
CN   10: PN: WO0100822 SEQID: 10 unclaimed protein (9CI)  (CA INDEX NAME)
CI   MAN
SQL  3096

SEQ      1 METGLGLPHE ASPLEVALLY STHRLEHISL YSTHRSERSE RSERVALGLY
        51 SERASPGLAS NSERLEHISS ERLEGLYLEA SNLEASNTHR ASPARGSERS
       101 ERPRHISLES ERTHRASNGL YVALSERSER PHESERGLYL YSTHRARGPR
       151 SERVALILEG LNGLYTHRVA LGLVALLETH RSERLEMETG LNGLLEGLNA
       201 SNSERGLYLY STHRASPSER GLLETRPLYS ASNCYSGLTH RARGTRPLEG
       251 LNLEPHEASN LEVALGLLYS GLNCYSGLNG LGLNILEVAL ALAGLNGLNG
       301 LGLNPHEHIS ASNGLNILEG LNHISILEGL NGLGLILELY SASNLEVALL
       351 YSLEGLNTHR SERSERALAS ERLEALASER CYSGLGLYAS NSERSERASN
       401 LYSGLNVALS ERSERGLSER GLNMETGLYP HEPHESERLE SERSERGLAR
       451 GASNGLSERV ALILEHISTY RPRGLSERTH RGLPRGLILE GLNGLNGLME
       501 TSERTHRSER GLNPRASPCY SASNVALASP SERCYSSERV ALSERSERGL
       551 YTYRGLYTHR PHECYSILES ERGLLEASNL ETYRLYSSER LYSASPPRLY
       601 SGLPHEMETG LHISILEASP VALPRLYSGL YGLNTYRVAL ALAPRALAVA
       651 LPRALAGLSE RLEVALASPG LYVALLYSAS NGLASNPHET YRILEGLNTH
       701 RPRGLGLCYS HISVALSERL ELYSGLASPV ALSERILESE RPRGLYGLPH
       751 EGLHISASNP HELEGLYGLA SNLYSVALSE RGLVALTYRS ERGLYLYSTH
       801 RASNSERASN ALAILETHRS ERTRPALAGL NLYSLELYSG LNASNGLNPR
       851 LYSARGALAH ISVALGLASP GLYGLYSERA RGSERLYSGL NGLYASNGLG
       901 LNSERLYSLY STHRPRILEG LLYSSERASP PHEALAALAA LATHRHISPR
       951 ARGALAPHET YRLESERLYS PRASPGLTHR PRASNALATR PMETSERASP
      1001 SERGLYTHRG LYLETHRTYR TRPLYSLEGL GLLYSASPME THISHISSER
      1051 LEPRGLTHRL EGLLYSTHRP HEILESERLE SERSERTHRA SPVALSERPR
      1101 ASNGLNVALL ETHRLEASPP RTHRLEHISM ETLYSPRLYS GLNGLNILES
      1151 ERGLYILEGL NPRHISGLYL EPRASNALAL EASPASPARG ILESERPHES
                                = =====
      1201 ERPRASPSER VALLEGLPRS ERMETSERSE RPRSERASPI LEASPSERPH
      1251 ESERGLNALA SERASNVALT HRSERGLNLE PRGLYPHEPR LYSTYRPRSE
      1301 RHISTHRLYS ALASERPRVA LASPSERTRP LYSASNGLNT HRPHEGLNAS
      1351 NGLSERARGT HRSERSERTH RPHEPRSERV ALTYRTHRIL ETHRSERASN
      1401 ASPILESERV ALASNTHRVA LASPGLGLAS NTHRVALMET VALALASERA
      1451 LASERVALSE RGLNSERGLN LEPRGLYTHR ALAASNSERV ALPRGLCYSI
      1501 LESERLETHR SERLEGLASP PRVALILELE SERLYSILEA RGGLNASNLE
      1551 LYSGLLYSHI SALAARGHIS ILEALAASPL EARGALATYR TYRGLSERGL
      1601 ILEASNSERL ELYSGLNLYS LEGLALALYS GLILESERGL YVALGLASPT
      1651 RPLYSILETH RASNGLNILE LEVALASPAR GCYSGLYGLN LEASPSERAL
      1701 ALEHISGLAL ATHRSERARG VALARGTHRL EGLASNLYSA SNASNLELEG
      1751 LILEGLVALA SNASPLEARG GLARGPHESE RALAALASER SERALASERL
      1801 YSILELEGLN GLARGILEGL GLMETARGTH RSERSERLYS GLLYSASPAS
      1851 NTHRILEILE ARGLELYSSE RARGLEGLNA SPLEGLGLAL APHEGLASNA
      1901 LATYRLYSLE SERASPASPL YSGLALAGLN LELYSGLNGL ASNLYSMETP
      1951 HEGLNASPLE LEGLYGLTYR GLSERLEGLY LYSGLHISAR GARGVALLYS
      2001 ASPALALEAS NTHRTHRGLA SNLYSLELEA SPALATYRTH RGLNILESER
      2051 ASPLELYSAR GMETILESER LYSLEGLALA GLNVALLYSG LNVALGLHIS
      2101 GLASNMETLE SERLEARGHI SASNSERARG ILEHISVALA RGPRSERARG
      2151 ALAASNTHRL EALATHRSER ASPVALSERA RGARGLYSTR PLEILEPRGL
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      2201 YALAGLTYRS ERILEPHETH RGLYGLNPRL EASPTHRGLN ASPSERASNV
      2251 ALASPASNGL NLEGLGLTHR CYSSERLEGL YHISARGSER PRLEGLLYSA
      2301 SPSERSERPR GLYSERSERS ERTHRSERLE LEILELYSLY SGLNARGGLT
      2351 HRSERASPTH RPRILEMETA RGALALELYS GLLEASPGLG LYLYSILEPH
      2401 ELYSASNTRP GLYTHRGLNT HRGLLYSGLA SPTHRSERAS NILEASNPRA
      2451 RGGLNTHRGL THRSERVALA SNALASERAR GSERPRGLLY SCYSALAGLN
      2501 GLNARGGLNL YSARGLEASN SERALASERG LNARGSERSE RSERLEPRPR
      2551 SERASNARGL YSSERSERTH RPRTHRLYSA RGGLILEMET LETHRPRVAL
      2601 THRVALALAT YRSERPRLYS ARGSERPRLY SGLASNLESE RPRGLYPHES
      2651 ERHISLELES ERLYSASNGL SERSERPRIL EARGPHEASP ILELELEASP
      2701 ASPLEASPTH RVALPRVALS ERTHRLEGLN ARGTHRASNP RARGLYSGLN
      2751 LEGLNPHELE PRLEASPASP SERGLGLLYS THRTYRSERG LLYSALATHR
      2801 ASPASNHISV ALASNHISSE RSERCYSPRG LPRVALPRAS NGLYVALLYS
      2851 LYSVALSERV ALARGTHRAL ATRPGLLYSA SNLYSSERVA LSERTYRGLG
      2901 LNCYSLYSPR VALSERVALT HRPRGLNGLY ASNASPPHEG LTYRTHRALA
      2951 LYSILEARGT HRLEALAGLT HRGLARGPHE PHEASPGLLE THRLYSGLLY
      3001 SASPGLNILE GLALAALALE SERARGMETP RSERPRGLYG LYARGILETH
      3051 RLEGLNTHRA RGLEASNGLN VALLYSCYSL ESERLEASNL ELEEND
HITS AT:   1170-1175

REFERENCE   1:  134:82484

L4   ANSWER 17 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   284706-28-1  REGISTRY
CN   Protein (Xylella fastidiosa gene XF1737) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AE003997-derived protein GI 9106807
CI   MAN
SQL  242

SEQ      1 MKPSRRSVLK SMGLLAAMPW LLPASRAFAA APMRIGVIGA GSLGGTVGRL
        51 WVKAGHEVMF SSRNPDKLEA MARELEPRAS VGQPLAATEF GTVLLLAVPF
                                   ======
       101 EALPQVGRDL RSAYRGKIVL DSTNPWGASS ADVYREAREL GVAQTVVKYM
       151 PGARLVRAFS AVDATVVETS ASRRGGRIGM PLASDDAEAM KVAEGLVRDA
       201 GCDPVIVGNL AAAASFQPGG PGFRAHLTAP ELRRRLGLPA AS
HITS AT:   75-80

REFERENCE   1:  133:130477

L4   ANSWER 18 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   263525-23-1  REGISTRY
CN   Protein (Drosophila melanogaster gene CG12263) (9CI)  (CA INDEX
     NAME)
OTHER NAMES:
CN   GenBank AE003799-derived protein GI 7302608
CI   MAN
SQL  1077

SEQ      1 MNLTYLFVLI WLAFLISSGV MLFSRGFLLA RVSKTETSTC RRLSTNPNAE
        51 YVLTDEVVNE IFKDVNASSN LCLPQKSKVI VLVVDALKYE FGLYRANATD
       101 PLPYENKLVV LQELLQQNPD HARLMRFRAD PPTTTLQRLK GLTTGSLPTF
       151 IDIGSNFASP EINEDNIIDQ IVKNDLPVVF LGDSTWTDLY PHRFKRSYSY
       201 PSFDIFDLDS VDNEILKHLP KELESKDWQV LVAHFLGVDH CGHKHGPMHE
       251 EMARKLGEMN EVIRSVVAAM DNDTTLLVMG DHGMTASGDH GGDTDDETNA
       301 LLFAYSKQHR FYGNDSGSDS EMLQQIDLVP TLATILGVPI PYSNLGLVNF
       351 NIVPDLRVPH LNKFQTLLLH SWQNAQQIYR YFFQYALENK RTFNVEQMDH
       401 LETEFILLTH RVQTVYNEVA FKSFVRDLNT NLRDILGTCR EIWVRFDPTQ
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       451 MSQGLLFTFL PLFFIFLVVN NSRPADFPHI FKAKEVFYVY LINLAAGVFG
       501 YRYFKTFSFK TEEQGVIFFT AISSAVILAF HTLRHWTSIA TNWSAVKRFG
       551 HMPTRLLLFG SMAVFFSNSF VIQEAKILSY LLAAAILLLS HELLRLSARL
       601 DFRTKFKASQ FLRSTALRLI LASVLAICLI RFAYTLFRCR EEQGNCSDFV
       651 NTGGAGFSLK KPGTGKTYIL AVVVLVVYTT LTRLYLRSCG NLTGNLPNVL
       701 LARYGPTVAS ICAGGHILLA NSSIKHIQRT HIDAMALVIY GLLLVQIIVL
       751 SWAPLMTFVL PPRSSHTVTI NGNESIVPEI FRKMKRMYEG DDDERRSHIP
       801 VVYGLATVYS SIVIAFGVFL ALVMIVLLEP RASIGLVVCV AVGAILLSVH
                                          === ===
       851 SILRYRTATS FESCVQPTFT ALVGWFLLAH FCFFATSHQT TLSQIEWRAA
       901 FVGRTTGIGQ SNLVSGALVI LNTFCGPIFF FCMYSLLSTE TFSLFALFPN
       951 LIRSCRSGGK VDASTSMSDL ANEAVGFDMT RGELSLYEYE DVFLGTGFKL
      1001 ATQFFMLQGL KIFCAMLACT IHCRHLMVWK IFAPRFIYEA LATFVSLPAL
      1051 IVGYLLVLRI HRGVDTLIKR INKAKVH
HITS AT:   828-833

REFERENCE   1:  132:275067

L4   ANSWER 19 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   262988-39-6  REGISTRY
CN   Protein (Drosophila melanogaster gene Mer) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AE003512-derived protein GI 7293633
CI   MAN
SQL  635

SEQ      1 MSPFGSKKNR SLSVRVSTFD SELEFKLEPR ASGQDLFDLV CRTIGLRESW
                                    ==== ==
         51 YFGLQYVDTR SNVSWLKMEK RVRDQRVELH ASNNVYVFSF YAKFFPENVS
        101 EELIQEITQH LFFLQVKQSI LSMDIYCRPE ASVLLASYAV HVQYGPYDYE
        151 TYKDGMLAGG ELLPKGVTDQ YQMTPEMWEE RIKTWYMDHE PMTRDEVEME
        201 YLKIAQDLDM YGVNYFPITN KNKTKLWLGV TSVGLNIYDE RDKLTPKTTF
        251 QWNEIRHVSF DDKKFTIRLV DAKVSNFIFY SQDLHINKMI LDLCKGNHDL
        301 YMRRRKPDTM EIQQMKAQAK EEKQRRQIER KKFIREKKLR EKAEHERYEL
        351 EKSMEHLQNE MRMANDALRR SEETKELYFE KSRVNEEQMQ LTECKANHFK
        401 TEMDRLRERQ MKIEREKHDL EKKIRDADFY VHQLTVENDK REAETEKLRK
        451 ELICAKMAER EATARLLEFL NSGRKSSTDS LLTASSVSHA ANTASSMAAI
        501 STPSLITSSS TNDLETAGGA ELTTHSSHYL VQGDNSSGIS DDFEPKEFIL
        551 TDNEMEQITN EMERNHLDYL RNSKQVQSQL QTLRSEIAPH KIEENQSNLD
        601 ILSEAQIKAG ENKYSTLKKL KSGSTKARVA FFEEL
HITS AT:   27-32

REFERENCE   1:  132:304167

L4   ANSWER 20 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   260386-80-9  REGISTRY
CN   Protein NMASP (Neisseria meningitidis) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   2: PN: WO0012535 SEQID: 2 claimed protein
CI   MAN
SQL  1253

SEQ      1 METLELEPRA SPPHEVALGL NLEVALGLNS ERGLGLYPRA LAVALVALAS
               ===== =
         51 NILEGLNALA ALAPRALAPR ARGTHRGLNA SNGLYSERSE RASNALAGLT
        101 HRASPSERAS PPRLEALAAS PSERASPPRP HETYRGLPHE PHELYSARGL
        151 EVALPRASNM ETPRGLILEP RGLNGLGLAL AASPASPGLY GLYLEASNPH
        201 EGLYSERGLY PHEILEILES ERLYSASPGL YTYRILELET HRASNTHRHI
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       251 SVALVALTHR GLYMETGLYS ERILELYSVA LLELEASNAS PLYSARGGLT
       301 YRTHRALALY SLEILEGLYS ERASPVALGL NSERASPVAL ALALELELYS
       351 ILEASPALAT HRGLGLLEPR VALVALLYSI LEGLYASNPR LYSASPLELY
       401 SPRGLYGLTR PVALALAALA ILEGLYALAP RPHEGLYPHE ASPASNSERV
       451 ALTHRALAGL YVALSERALA LYSGLYARGS ERLEPRASNG LSERTYRTHR
                                                   ======
       501 PRPHEILEGL NTHRASPVAL ALAILEASNP RGLYASNSER GLYGLYPRLE
       551 PHEASNLELY SGLYGLNVAL VALGLYILEA SNSERGLNIL ETYRSERARG
       601 SERGLYGLYP HEMETGLYIL ESERPHEALA ILEPRILEAS PVALALAMET
       651 ASNVALALAG LGLNLELYSA SNTHRGLYLY SVALGLNARG GLYGLNLEGL
       701 YVALILEILE GLNGLVALSE RTYRGLYLEA LAGLNSERPH EGLYLEASPL
       751 YSALAGLYGL YALALEILEA LALYSILELE PRGLYSERPR ALAGLARGAL
       801 AGLYLEARGA LAGLYASPIL EVALLESERL EASPGLYGLY GLILEARGSE
       851 RSERGLYASP LEPRVALMET VALGLYALAI LETHRPRGLY LYSGLVALSE
       901 RLEGLYVALT RPARGLYSGL YGLGLILETH RILELYSVAL LYSLEGLYAS
       951 NALAALAGLH ISILEGLYAL ASERSERLYS THRASPGLAL APRTYRTHRG
      1001 LGLNGLNSER GLYTHRPHES ERVALGLSER ALAGLYILET HRLEGLNTHR
      1051 HISTHRASPS ERSERGLYGL YHISLEVALV ALVALARGVA LSERASPALA
      1101 ALAGLARGAL AGLYLEARGA RGGLYASPGL ILELEALAVA LGLYGLNVAL
      1151 PRVALASNAS PGLALAGLYP HEARGLYSAL AMETASPLYS ALAGLYLYSA
      1201 SNVALPRLEL EILEMETARG ARGGLYASNT HRLEPHEILE ALALEASNLE
      1251 GLN
HITS AT:   6-11, 483-488

REFERENCE   1:  132:204089

L4   ANSWER 21 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   253582-33-1  REGISTRY
CN   Tumor suppressor protein (human gene AZ-2) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   4: PN: WO0000503 SEQID: 4 claimed protein
CI   MAN
SQL  1219

SEQ      1 GTSDSPHGRR WSWDFAHTGV PGHVPRSTCA PSPQREVLTV PEANSEPWTL
        51 DTLGGERRPG VTAGILEMRN ALGNQSTPAP PTGEVADTPL EPGKVAGAAG
       101 EAEGDITLST AETQACASGD LPEAGTTRTF SVVAGDLVLP GSCQDPACSD
       151 KAPGMEGTAA LHGDSPARPQ QDKEQPGPER PIPAGDGKVC VSSPPEPDET
       201 HDPKLQHLAP EELHTDRESP RPGPSMLPSV PKKDAPRVMD KVTSDETRGA
       251 EGTESSPVAD DIIQPAAPAD LESPTLAASS YHSDVVGQVS TDLIAQRSSD
       301 SEEAFETPES TTPVKAPPAP PPPPPEVIPE PEVSTQPPPE EPGCGSETVP
       351 VPDGPRSDSV EGSPFRPPSH PFSAVFDEDQ PIASSGTYNL DFDNIELVDT
       401 FQTLEPRASD AKNQEGKVNT RRKSTDSVPI SKSTLSRSLS LQASDFDGAS
             ======
       451 SSGNPEAVAL APDAYSTGSS SASSTLKRTK KPRPPSLKKK QTTKKPTETP
       501 PVKETQQEPD EESLVPSGEN LASETKTESA KTEGPSPALL EETPLEPAVG
       551 PKAACPLDSE SAEGVVPPAS GGGRVQNSPP VGRKTLPLTT APEAGEVTPS
       601 DSGGQEDSPA KGLSVRLEFD YSEDKSSWDN QQENPPPTKK IGKKPVAKMP
       651 LRRPKMKKTP EKLDNTPASP PRSPAEPNDI PIAKGTYTFD IDKWDDPNFN
       701 PFSSTSKMQE SPKLPQQSYN FDPDTCDESV DPFKTSSKTP SSPSKSPASF
       751 EIPASAMEAN GVDGDGLNKP AKKKKTPLKT VKKSPKRSPL SDPPSQDPTP
       801 AATPETPPVI SAVVHATDEE KLAVTNQKWT CMTVDLEADK QDYPQPSDLS
       851 TFVNETKFSS PTEELDYRNS YEIEYMEKIG SSLPQDDDAP KKQALYLMFD
       901 TSQESPVKSS PVRMSESPTP CSGSSFEETE ALVNTAAKNQ HPVPRGLAPN
       951 QESHLQVPEK SSQKELEAMG LGTPSEAIEI REAAHPTDVS ISKTALYSRI
      1001 GTAEVEKPAG LLFQQPDLDS ALQIARAEII TKEREVSEWK DKYEESRREV
      1051 MEMRKIVAEY EKTIAQMIED EQREKSVSHQ TVQQLVLEKE QALADLNSVE
      1101 KSLADLFRRY EKMKEVLEGF RKNEEVLKRC AQEYLSRVKK EEQRYQALKV
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      1151 HAEEKLDRAN AEIAQVRGKA QQEQAAHQAS LRKEQLRVDA LERTLEQKNK
      1201 EIEELTKICD ELIAKMGKS
HITS AT:    404-409

REFERENCE   1:  132:74540

L4    ANSWER 22 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN    250313-43-0  REGISTRY
CN    Protein (Deinococcus radiodurans strain R1 gene DR1748) (9CI)  (CA
      INDEX NAME)
OTHER NAMES:
CN    GenBank AE002016-derived protein GI 6459525
CI    MAN
SQL   162

SEQ       1 MHPGPAILPF MDDLIQGRLG GADGYDIRCT IDGDKISGRA GGKLHGKDIE
         51 LEITDRGVRG SVGQESVNIE LQEGELRGNV GSQKLVLRGV DRVTGFMGEP
        101 IVGWNIVAQQ QGESLQGQLG STVLGRVFSL DLGSAPGWVG TLVAVVAFYA
        151 LEPRASMGAQ AS
            ======
HITS AT:    151-156

REFERENCE   1:  131:347336

L4    ANSWER 23 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN    244613-54-5  REGISTRY
CN    Myosin (human clone BACMYO1/BACMYO2 gene MYO9A isoform IXA) (9CI)
      (CA INDEX NAME)
OTHER NAMES:
CN    GenBank AF117888-derived protein GI 5732618
CN    Myosin IXA (human clone BACMYO1/BACMYO2 gene MYO9A)
CI    MAN
SQL   2548

SEQ       1 MNINDGGRRR FEDNEHTLRI YPGAISEGTI YCPIPARKNS TAAEVIESLI
         51 NKLHLDKTKC YVLAEVKEFG GEEWILNPTD CPVQQMMLWP RMALENRLSG
        101 EDYRFLLREK NLDGSIHYGS LQSWLRVTEE RRRMMERGFL PQPQQKDFDD
        151 LCSLPDLNEK TLLENLRDRF KHEKIYTYVG SILIVINPFK FLPIYNPKYV
        201 KMYDNHQLGK PEPHIYAVAD VAYHAMLQRK KNQCIVISGE SGSGKTQSTN
        251 FLIHHLTALS QKGFASGVEQ IILGAGPVLE AFGNAKTAHN NNSSRFGKFI
        301 QVNYQETGTV LGAYVEKYLL EKSRLVYQEH NERNYHVFYY LLAGASEDER
        351 SAFHLKQPEE YHYLNQITKK PLRQSWDDYC YDSEPDCFTV EGEDLRHDFE
        401 RLQLAMEMVG FLPKTRRQIF SLLSAILHLG NICYKKKTYR DDSIDICNPE
        451 VLPIVSELLE VKEEMLFEAL VTRKTVTVGE KLILPYKLAE AVTVRNSMAK
        501 SLYSALFDWI VFRINHALLN SKDLEHNTKT LSIGVLDIFG FEDYENNSFE
        551 QFCINFANER LQHYFNQHIF KLEQEEYRTE GISWHNIDYI DNTCCINLIS
        601 KKPTGLLHLL DEESNFPQAT NQTLLDKFKH QHEDNSYIEF PAVMEPAFII
        651 KHYAGKVKYG VKDFREKNTD HMRPDIVALL RSSKNAFISG MIGIDPVAVF
        701 RWAILRAFFR AMVAFREAGK RNIHRKTGHD DTAPCAILKS MDSFSFLQHP
        751 VHQRSLEILQ RCKEEKYSIT RKNPRTPLSD LQGMNALNEK NQHDTFDIAW
        801 NGRTGIRQSR LSSGTSLLDK DGIFANSTSS KLLERAHGIL TRNKNFKSKP
        851 ALPKHLLEVN SLKHLTRLTL QDRITKSLLH LHKKKKPPSI SAQFQASLSK
        901 LMETLGQAEP YFVKCIRSNA EKLPLRFSDV LVLRQLRYTG MLETVQIRQS
        951 GYSSKYSFQD FVSHFHVLLP RNIIPSKFNI QDFFRKINLN PDNYQVGKTM
       1001 VFLKEQERQH LQDLLHQEVL RRIILLQRWF RVLLCRQHFL HLRQASVIIQ
       1051 RFWRNYLNQK QVRDAAVQKD AFVMASAAAL LQASWRAHLE RQRYLELRAA
       1101 AIVIQQKWRD YYRRRHMAAI CIQARWKAYR ESKRYQEQRK KIILLQSTCR
       1151 GFRARQRFKA LKEQRLRETK PEVGLVNIKG YGSLEIQGSD PSEWEDCSFD
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      1201 NRIKAIEECK SVIESNRISR ESSVDCLKES PNKQQERAQS QSGVDLQEDV
      1251 LVRERPRSLE DLHQKKVGRA KRESRRMREL EQAIFSLELL KVRSLGGISP
      1301 SEDRRWSTEL VPEGLQSPRG TPDSESSQGS LELLSYEESQ KSKLESVISD
      1351 EGDLQFPSPK ISSSPKFDSR DNALSASNET SSAEHLKDGT MKEMVVCSSE
      1401 SITCKPQLKD SFISNSLPTF FYIPQQDPLK TNSQLDTSIQ RNKLLENEDT
      1451 AGEALTLDIN RETRRYHCSG KDQIVPSLNT ESSNPVLKKL EKLNTEKEER
      1501 QKQLQQQNEK EMMEQIRQQT DILEKERKAF KTIEKPRIGE CLVAPSSYQS
      1551 KQRVERPSSL LSLNTSNKGE LNVLGSLSLK DAALAQKDSS SAHLPPKDRP
      1601 VTVFFERKGS PCQSSTVKEL SKTDRMGTQL NVACKLSNNR ISKREHFRPT
      1651 QSYSHNSDDL SREGNARPIF FTPKDNMSIP LVSKEALNSK NPQLHKEDEP
      1701 AWKPVKLAGP GQRETSQRFS SVDEQAKLHK TMSQGEITKL AVRQKASDSD
      1751 IRPQRAKMRF WAKGKQGEKK TTRVKPTTQS EVSPLFAGTD VIPAHQFPDE
      1801 LAAYHPTPPL SPELPGSCRK EFKENKEPSP KAKRKRSVKI SNVALDSMHW
      1851 QNDSVQIIAS VSDLKSMDEF LLKKVNDLDN EDSKKDTLVD VVFKKALKEF
      1901 RQNIFSFYSS ALAMDDGKSI RYKDLYALFE QILEKTMRLE QRDSLGESPV
      1951 RVWVNTFKVF LDEYMNEFKT SDCTATKVPK TERKKRRKKE TDLVEEHNGH
      2001 IFKATQYSIP TYCEYCSSLI WIMDRASVCK LCKYACHKKC CLKTTAKCSK
      2051 KYDPELSSRQ FGVELSRLTS EDRTVPLVVE KLINYIEMHG LYTEGIYRKS
      2101 GSTNKIKELR QGLDTDAESV NLDDYNIHVI ASVFKQWLRD LPNPLMTFEL
      2151 YEEFLRAMGL QERKETIRGV YSVIDQLSRT HLNTLERLIF HLVRIALQED
      2201 TNRMSANALA IVFAPCILRC PDTTDPLQSV QDISKTTTCV ELIVVEQMNK
      2251 YKARLKDISS LEFAENKAKT RLSLIRRSMG KGRIRRGNYP GPSSPVVVRL
      2301 PSVSDVSEET LTSEAAMETD ITEQQQAAMQ QEERVLTEQI ENLQKEKEEL
      2351 TFEMLVLEPR ASDDETLESE ASIGTADSSE NLNMESEYAI SEKSERSLAL
                ==== ==
      2401 SSLKTAGKSE PSSKLRKQLK KQQDSLDVVD SSVSSLCLSN TASSHGTRKL
      2451 FQIYSKSPFY RAASGNEALG MEGPLGQTKF LEDKPQFISR GTFNPEKGKQ
      2501 KLKNVKNSPQ KTKETPEGTV MSGRRKTVDP DCTSNQQLAL FGNNEFMV
HITS AT:    2357-2362

REFERENCE   1:  131:253834

L4    ANSWER 24 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN    222964-43-4  REGISTRY
CN    Myosin IXa (human clone BAC) (9CI)  (CA INDEX NAME)
CI    MAN
SQL   2548

SEQ       1 MNINDGGRRR FEDNEHTLRI YPGAISEGTI YCPIPARKNS TAAEVIESLI
         51 NKLHLDKTKC YVLAEVKEFG GEEWILNPTD CPVQQMMLWP RMALENRISG
        101 EDYRFLLREK NLDGSIHYGS LQSWLRVTEE RRRMMERGFL PQPQQKDFDD
        151 LCSLPDLNEK TLLENLRDRF KHEKIYTYVG SILIVINPFK FLPIYNPKYV
        201 KMYDNHQLGK PEPHIYAVAD VAYHAMLQRK KNQCIVISGE SGSGKTQSTN
        251 FLIHHLTALS QKGFASGVEQ IILGAGPVLE AFGNAKTAHN NNSSRFGKFI
        301 QVNYQETGTV LGAYVEKYLL EKSRLVYQEH NERNYHVFYY LLAGASEDER
        351 SAFHLKQPEE YHYLNQITKK PLRQSWDDYC YDSEPDCFTV EGEDLRHDFE
        401 RLQLAMEMVG FLPKTRRQIF SLLSAILHLG NICYKKKTYR DDSIDICNPE
        451 VLPIVSELLE VKEEMLFEAL VTRKTVTVGE KLILPYKLAE AVTVRNSMAK
        501 SLYSALFDWI VFRINHALLN SKDLEHNTKT LSIGVLDIFG FEDYENNSFE
        551 QFCINFANER LQHYFNQHIF KLEQEEYRTE GISWHNIDYI DNTCCINLIS
        601 KKPTGLLHLL DEESNFPQAT NQTLLDKFKH QHEDNSYIEF PAVMEPAFII
        651 KHYAGKVKYG VKDFREKNTD HMRPDIVALL RSSKNAFISG MIGIDPVAVF
        701 RWAILRAFFR AMVAFREAGK RNIHRKTGHD DTAPCAILKS MDSFSFLQHP
        751 VHQRSLEILQ RCKEEKYSIT RKNPRTPLSD LQGMNALNEK NQHDTFDIAW
        801 NGRTGIRQSR LSSGTSLLDK DGIFANSTSS KLLERAHGIL TRNKNFKSKP
        851 ALPKHLLEVN SLKHLTRLTL QDRITKSLLH LHKKKKPPSI SAQFQASLSK
        901 LMETLGQAEP YFVKCIRSNA EKLPLRFSDV LVLRQLRYTG MLETVQIRQS
        951 GYSSKYSFQD FVSHFHVLLP RNIIPSKFNI QDFFRKINLN PDNYQVGKTM
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      1001 VFLKEQERQH LQDLLHQEVL RRIILLQRWF RVLLCRQHFL HLRQASVIIQ
      1051 RFWRNYLNQK QVRDAAVQKD AFVMASAAAL LQASWRAHLE RQRYLELRAA
      1101 AIVIQQKWRD YYRRRHMAAI CIQARWKAYR ESKRYQEQRK KIILLQSTCR
      1151 GFRARQRFKA LKEQRIRETK PEVGLVNIKG YGSLEIQGSD PSEWEDCSFD
      1201 NRIKAIEECK SVIESNRISR ESSVDCLKES PNKQQERAQS QSGVDLQEDV
      1251 LVRERPRSLE DLHQKKVGRA KRESRRMREL EQAIFSLELL KVRSLGGISP
      1301 SEDRRWSTEL VPEGLQSPRG TPDSESSQGS LELLSYEESQ KSKLESVISD
      1351 EGDLQFPSPK ISSSPKFDSR DNALSASNET SSAEHLKDGT MKEMVVCSSE
      1401 SITCKPQLKD SFISNSLPTF FYIPQQDPLK TNSQLDTSIQ RNKLLENEDT
      1451 AGEALTLDIN RETRRYHCSG KDQIVPSLNT ESSNPVLKKL EKLNTEKEER
      1501 QKQLQQQNEK EMMEQIRQQT DILEKERKAF KTIEKPRIGE CLVAPSSYQS
      1551 KQRVERPSSL LSLNTSNKGE LNVLGSLSLK DAALAQKDSS SAHLPPKDRP
      1601 VTVFFERKGS PCQSSTVKEL SKTDRMGTQL NVACKLSNNR ISKREHFRPT
      1651 QSYSHNSDDL SREGNARPIF FTPKDNMSIP LVSKEALNSK NPQLHKEDEP
      1701 AWKPVKLAGP GQRETSQRFS SVDEQAKLHK TMSQGEITKL AVRQKASDSD
      1751 IRPQRAKMRF WAKGKQGEKK TTRVKPTTQS EVSPLFAGTD VIPAHQFPDE
      1801 LAAYHPTPPL SPELPGSCRK EFKENKEPSP KAKRKRSVKI SNVALDSMHW
      1851 QNDSVQIIAS VSDLKSMDEF LLKKVNDLDN EDSKKDTLVD VVFKKALKEF
      1901 RQNIFSFYSS ALAMDDGKSI RYKDLYALFE QILEKTMRLE QRDSLGESPV
      1951 RVWVNTFKVF LDEYMNEFKT SDCTATKVPK TERKKRRKKE TDLVEEHNGH
      2001 IFKATQYSIP TYCEYCSSLI WIMDRASVCK LCKYACHKKC CLKTTAKCSK
      2051 KYDPELSSRQ FGVELSRLTS EDRTVPLVVE KLINYIEMHG LYTEGIYRKS
      2101 GSTNKIKELR QGLDTDAESV NLDDYNIHVI ASVFKQWLRD LPNPLMTFEL
      2151 YEEFLRAMGL QERKETIRGV YSVIDQLSRT HLNTLERLIF HLVRIALQED
      2201 TNRMSANALA IVFAPCILRC PDTTDPLQSV QDISKTTTCV ELIVVEQMNK
      2251 YKARLKDISS LEFAENKAKT RLSLIRRSMG KGRIRRGNYP GPSSPVVVRL
      2301 PSVSDVSEET LTSEAAMETD ITEQQQAAMQ QEERVLTEQI ENLQKEKEEL
      2351 TFEMLVLEPR ASDDETLESE ASIGTADSSE NLNMESEYAI SEKSERSLAL
                ==== ==
      2401 SSLKTAGKSE PSSKLRKQLK KQQDSLDVVD SSVSSLCLSN TASSHGTRKL
      2451 FQIYSKSPFY RAASGNEALG MEGPLGQTKF LEDKPQFISR GTFNPEKGKQ
      2501 KLKNVKNSPQ KTKETPEGTV MSGRRKTVDP DCTSNQQLAL FGNNEFMV
HITS AT:    2357-2362

REFERENCE   1:  130:292458

L4   ANSWER 25 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   221651-87-2  REGISTRY
CN   GTPase-activating protein Myr-7 (Rattus norvegicus gene myo9a Rho
     protein-specific) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AJ001713-derived protein GI 3955026
CN   Myosin-RhoGAP protein Myr 7 (rat gene myo9a)
CI   MAN
SQL  2626

SEQ       1 MNVSDGGRRR FEDNEHTLRI YPGTISEGTI YCPIPARKNS TAAEVIDSLI
         51 NRLHLDKTKC YVLAEVKEFG GEEWILNPTD CPVQRMMLWP RMALENRLSG
        101 EDYRFLLREK NLDGSIHYGS LQSWLRVTEE RRRMMERGFL PQPQQKDFDD
        151 LCSLPDLNEK TLLENLRNRF KHEKIYTYVG SILIAINPFK FLPIYNPKYV
        201 KMYDNHQLGK LEPHIYAVAD VAYHAMLQRK KNQCIVISGE SGSGKTQSTN
        251 FLIHHLTALS QKGFASGVEQ IILGAGPVLE AFGNAKTAHN NNSSRFGKFI
        301 QVNYQETGTV LGAYVEKYLL EKSRLVYQEH NERNYHVFYY LLAGASEEER
        351 LAFHLKQPEE YHFLNQITKK PLRQSWDDYC YDSEPDCFTV EGEDLRHDFE
        401 RLQLAMEMVG FLPKTRRQIF SLLSAILHLG NISYKKKTYR DDSIDICNPE
        451 VLPIVSELLE VKEEMLFEAL VTRKTVTVGE KLILPYKLAE AVTVRNSMAK
        501 SLYSALFDWI VFRINHALLN SKDLEKDTKT LSIGVLDIFG FEDYENNSFE
        551 QFCINFANER LQHYFNQHIF KLEQEEYRTE GISWHNIDYI DNTCCINLIS
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         601 KKPTGLLHLL DEESNFPQAT NQTLLDKFKH QHEENSYIEF PAVMEPAFII
         651 KHYAGKVKYG VKDFREKNTD HMRPDIVALL RSSRNAFVSG MTGIDPVAVF
         701 RWAVLRAFFR AVVAFREAGK RHIQRKSGHD DTTPCTILKS MDSFSFLQHP
         751 VHQRSLEILQ RCKEEKYSIT RKNPRTPLSD LQGMNTLNEK NQHDTFDIAW
         801 NVRTGIRQSR LPTNNTSLLD KDGIFANSAS SKLLERAHGI LTRNKNFRSK
         851 PVLPKHLLEV NSLKHLTRLT LQDRITKSLL HLHKKKKPPS ISAQFQVSLS
         901 KLMETLDQAE PYFVKCIRSN AEKLPLRFSD ALVLRQLRYT GMLETVRIRQ
         951 SGYSSKYSFQ DFVSHFHVLL PQHIIPSKFN IQDFFRKINI NPDNYQVGKT
        1001 MVFLKEHERQ HLQDLLHQEV LRRIILLQRW FRVLLSRQQF LHLRQASVII
        1051 QRFWRNYLNQ KQVRNAAVEK DAFIMASAAS LLQASWRAHL ERQRYLELRA
        1101 AAVIIQQRWR ELCRRRHRAA TCIQSRWRGY RQSKKYKEQR NKIILLQSIY
        1151 RGFRARQRYK ALKEERLKET KLEHGLAQIK TCGPLEIQGS DPSEWEDRSF
        1201 ANRVKAIEEC KSVIESNRIS RESSMDFSKE SPDKQQERGR SQSGTDLQGD
        1251 VIVRQRPKSL EDLHQKKVGR AKRESRRMRE LEQAIFSLEL LKVRSLGGMS
        1301 PSEERRWSTE LMPEGLQSPQ GTPDSESSQG SLELLTCDEN QKSKPESLIL
        1351 DDGELKISSP STFTNPKFDS QNNALSASSE TSSTFSGKGA SSDSEHLKNG
        1401 TAEEKLVYSS QPITCKSQLR DSFVSSSLPT FFYIPHQEPL KTSSQLDTSI
        1451 QRNKLPERET TLKTTLTLDI NREARKCQFS GQVTPLNPDS SCTVLKKLEK
        1501 LNIEKEKRQK QLQQQNEKEM MEQIRQQTDI LEKERKAFKT IEQSRTEASL
        1551 LAPSFYQSRQ KVERPSSLHI QNTPSKGEAG VLGSPSALAT KDSPSIHLPP
        1601 KDRPVTLFFE RKGSPCQSRT VKELTKTERM GTQHDAACRL SNNHNTEREH
        1651 FKSTHSYSHR SDDPSREGSS RPIFFTPKDN VITPLVHSGN PQVHKQDEPA
        1701 WKSKLAGPGQ REVARPAHKK KARMARTRSD FLTRGTFADG EGDTEEDDYD
        1751 DIIEPLLSLD QASHSELGPV SSLGQASHSD SEMTSQRFSS VDEQARLHKA
        1801 MSQGEITKLA GRQKSSDLDI RPQRAKMRFW AKGKQGEKKT TRVKPAPQSE
        1851 VSSLFAGSDV TPVHPFSDEL TQYHPTPPLS PELPGSCRKE FKENKEPSPK
        1901 AKRKRGVKIS SVALDSMHWQ NDSVQIIASA NDLKSMDEFL LKKMNDLDNE
        1951 DSKKDTLVDV VFKKALKEFR QNIFSSYSSA LAMDDGKSIR YKDLYALFEQ
        2001 ILEKTMRFEQ RDWNESPVRV WVNTFKVFLD EYMNEFKTLD STAPKVLKTE
        2051 RKKRRKKETD LVEEHNGHMF KATQYSIPTY CEYCSSLIWI MDRASVCKLC
        2101 KYACHKKCCL KTTAKCSKKY DPELSSRQFG VELSRLTSED RAVPLVVEKL
        2151 INYIEMHGLY TEGIYRKSGS TNKIKELRQG LDTDAESVNL DDYNIHVIAS
        2201 VFKQWLRDLP NPLMTFELYE EFLRAMGLQE RKETIRGVYS VIDQLSRTHL
        2251 STLERLIFHL VRIALQEDTN RMSANALAIV FAPCILRCPD TTDPLQSVQD
        2301 ISKTTTCVEL IVVEQMNKYK ARLKDISSLE FAENKAKTRL SLIRRSMKPV
        2351 LIAVRFMSIT RSSVSGKGRL HRGSHPNPSS PVIVRLPSMS DVPEETLTSE
        2401 TAMDTDVTDQ QQAAMQQEEK VLTEQIENLQ KEKEELTFEM LVLEPRASDD
                                                      ======
        2451 EALESEASIG TADSSENLNM DPEERSLALS SLKAAGKSEP SSKFRKQLRK
        2501 QPDSLDSVSS SVSSCLSNTT SSHGTRKRFQ IYSKSPFYRA ASACEAQGME
        2551 GPLGQAKSLE DRPQFISRGT FNPEKGKQKL KNVKNSPQKT KETPEGTVSS
        2601 GRKKTVDSDC SSTQQLPLFG NNEFMV
HITS AT:    2443-2448

REFERENCE   1:  130:265212

L4    ANSWER 26 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN    218778-68-8  REGISTRY
CN    178-273-Protein Zneu1 (human neuro-growth factor-like fragment)
      (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN    Protein Zneu1 (human neuro-growth factor-like HSMHC3W5A-like (HSM2)
      domain)
CI    MAN
SQL   256

SEQ       1 PRLYSGLYGL YPRPRARGVA LALAPRASNP RTHRGLYVAL ASPSERALAM
         51 ETLYSGLGLV ALGLNARGLE GLNSERARGV ALASPLELEG LGLLYSLEGL
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       101 NLEVALLEAL APRLEHISSE RLEALASERG LNALALEGLH ISGLYLEPRA
                                                          =====
       151 SPPRGLYSER LELEVALHIS SERPHEGLNG LNLEGLYARG ILEASPSERL
           =
       201 ESERGLGLNI LESERPHELE GLGLGLNLEG LYSERCYSSE RCYSLYSLYS
       251 ASPSER
HITS AT:   146-151

REFERENCE   1:  130:77730

L4   ANSWER 27 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   218778-65-5  REGISTRY
CN   20-104-Protein Zneu1 (human neuro-growth factor-like fragment) (9CI)
     (CA INDEX NAME)
OTHER NAMES:
CN   Protein Zneu1 (human neuro-growth factor-like HSMHC3W5A-like (HSM1)
     domain)
CI   MAN
SQL  708

SEQ      1 THRGLHISAL ATYRARGPRG LYARGARGVA LCYSALAVAL ARGALAHISG
        51 LYASPPRVAL SERGLSERPH EVALGLNARG VALTYRGLNP RPHELETHRT
       101 HRCYSASPGL YHISARGALA CYSSERTHRT YRARGTHRIL ETYRARGTHR
       151 ALATYRARGA RGSERPRGLY LEALAPRALA ARGPRARGTY RALACYSCYS
       201 PRGLYTRPLY SARGTHRSER GLYLEPRGLY ALACYSGLYA LAALAILECY
       251 SGLNPRPRCY SARGASNGLY GLYSERCYSV ALGLNPRGLY ARGCYSARGC
       301 YSPRALAGLY TRPARGGLYA SPTHRCYSGL NSERASPVAL ASPGLCYSSE
       351 RALAARGARG GLYGLYCYSP RGLNARGCYS VALASNTHRA LAGLYSERTY
       401 RTRPCYSGLN CYSTRPGLGL YHISSERLES ERALAASPGL YTHRLECYSV
       451 ALPRLYSGLY GLYPRPRARG VALALAPRAS NPRTHRGLYV ALASPSERAL
       501 AMETLYSGLG LVALGLNARG LEGLNSERAR GVALASPLEL EGLGLLYSLE
       551 GLNLEVALLE ALAPRLEHIS SERLEALASE RGLNALALEG LHISGLYLEP
                                                          ===
       601 RASPPRGLYS ERLELEVALH ISSERPHEGL NGLNLEGLYA RGILEASPSE
           ===
       651 RLESERGLGL NILESERPHE LEGLGLGLNL EGLYSERCYS SERCYSLYSL
       701 YSASPSER
HITS AT:   598-603

REFERENCE   1:  130:77730

L4   ANSWER 28 OF 28  REGISTRY  COPYRIGHT 2002 ACS
RN   178535-96-1  REGISTRY
CN   Merlin (Drosophila melanogaster moesin-ezrin-radixin-like) (9CI)
     (CA INDEX NAME)
CI   MAN
SQL  636

SEQ      1 MSPFGSKKNR SLSVRVSTFD SELEFKLEPR ASGQDLFDLV CRTIGLRESW
                                   ====  ==
        51 YFGLQYVDTR SNVSWLKMEK RVRDQRVELH ASNNVYVFSF YAKFFPENVS
       101 EELIQEITQH LFFLQVKQSI LSMDIYCRPE ASVLLASYAV HVQYGPYDYE
       151 TYKDGMLAGG ELLPKGVTDQ YQMTPEMWEE RIKTWYMDHE PMTRDEVEME
       201 YLKIAQDLDM YGVNYFPITN KNKTKLWLGV TSVGLNIYDE RDKLTPKTTF
       251 QWNEIRHVSF DDKKFTIRLV DAKVSNFIFY SQDLHINKMI LDLCKGNHDL
       301 YMRRRKPDTM EIQQMKAQAK EEKQRRQIER KKFIREKKLR EKAEHERYEL
       351 EKSMEHLQNE MRMANDALRR SEETKELYFE KSRVNEEQMQ LTECKANHFK
       401 TEMDRLRERQ MKIEREKHDL EKKIRDADFY VHQLTVENDK REAETEKLRK
```

451 ELICAKMAER EATARLLEFL NSGRKSSTDS LLTASSVSHA ANTASSMAAI
501 STPSLITSSS TNDLETAGGA ELTTHSSHYL VQGDNSSGIS DDFEPKEFIL
551 TDNEMEQITN EMERNHLDYL RNSKQVQSQL QTLRSEIAPH KIEENQSNLD
601 ILSEAQIKAG ENKYSTLKKL KSGSTKARVA FFEELX
HITS AT: 27-32

REFERENCE 1: 125:82238

-key terms

(FILE 'HCAPLUS' ENTERED AT 15:42:25 ON 07 JUN 2002)
L5 6517 SEA FILE=HCAPLUS ABB=ON PLU=ON GFP(S)GREEN OR GREEN FLUORESC? PROTEIN
L6 1795 SEA FILE=HCAPLUS ABB=ON PLU=ON L5 AND (MUTAT? OR MUTAGEN? OR MUTANT OR POLYMORPH? OR POLY MORPH?)
L7 5 SEA FILE=HCAPLUS ABB=ON PLU=ON L6 AND (SER147PRO OR ((SER OR SERINE)(S)147 OR SER147 OR SERINE147)(S)(PRO OR PROLINE) OR SERINE147PROLINE)

L8 5 L7 NOT L2

L8 ANSWER 1 OF 5 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:187032 HCAPLUS
TITLE: Why do folding **mutations** decrease the thermosensitivity of **Green Fluorescent Proteins**?
AUTHOR(S): Zimmer, Marc; Fedeles, Flavia
CORPORATE SOURCE: Chemistry, Connecticut College, New London, CT, 06320, USA
SOURCE: Abstracts of Papers, 223rd ACS National Meeting, Orlando, FL, United States, April 7-11, 2002 (2002), CHED-401. American Chemical Society: Washington, D. C.
CODEN: 69CKQP
DOCUMENT TYPE: Conference; Meeting Abstract
LANGUAGE: English
AB **Green Fluorescent Protein** is a spontaneously fluorescent sol. globular protein isolated from jellyfish (Aequorea victoria). The efficiency with which newly synthesized GFP folds into the fluorescent active form is temp. dependent, which causes difficulty in the use of GFP. Recently it was shown that **mutation** of the **serine** residue at position **147** to a **proline** results in a redn. of the temp. sensitivity of GFP. The **mutated** variant is able to efficiently maturate at temps. as high as 37 .degree.C. We have attempted to det. through computational methods whether the lower thermosensitivity of the S147P **mutant** is due to a better folding of the b-sheets in the b barrel of GFP and therefore to a tighter folding of the residues around the chromophore region of GFP. Our results show that there is no significant difference between the folding pattern of the b-barrel in the wild-type and **mutant** GFP but the chromophore region is more tightly preorganized for autocatalytic cyclization in the S147P **mutant.**

L8 ANSWER 2 OF 5 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:473042 HCAPLUS
DOCUMENT NUMBER: 135:89517
TITLE: A bioluminescence resonance energy transfer (BRET) system with broad spectral resolution

between donor and acceptor emission wavelengths and its use
INVENTOR(S): Joly, Erik
PATENT ASSIGNEE(S): Biosignal Packard Inc., Can.
SOURCE: PCT Int. Appl., 132 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001046691	A1	20010628	WO 2000-CA1516	20001222

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: CA 1999-2291968 A 19991222
CA 2000-2314861 A 20000802

AB The present invention provides a bioluminescence resonance energy transfer (BRET) detection system characterized by a broad spectral resoln. between donor and acceptor emission wavelengths. The broad spectral resoln. between the emission wavelength of the bioluminescent donor protein and the fluorescent acceptor mol. results in an increased signal-to-base ratio and dynamic range in comparison with a basic BRET system. A BRET apoptosis sensor was prepd. by recombinantly prepg. **mutant green fluorescent protein** GFP1 fused with a linker peptide contg. a caspase-3 cleavage site and fused with **mutant** Renilla luciferase (Rluc). Upon induction of apoptosis, caspase-3 cleaves the linker, sepg. the GFP1 from Rluc causing the BRET ratio to decrease over time.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 3 OF 5 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:324955 HCAPLUS
DOCUMENT NUMBER: 131:155431
TITLE: S147P **green fluorescent protein**: a less thermosensitive **green fluorescent protein** variant
AUTHOR(S): Kimata, Yukio; Lim, Chun Ren; Kohno, Kenji
CORPORATE SOURCE: Research and Education Center for Genetic Information, Nara Institute of Science and Technology, Nara, 630-01, Japan
SOURCE: Methods in Enzymology (1999), 302(Green Fluorescent Protein), 373-378
CODEN: MENZAU; ISSN: 0076-6879

PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A new **green fluorescent protein** (**GFP**) variant is described in which **serine-147** is **mutated** to **proline**. The S147P **mutation** alters the maturation efficiency of GFP at 37.degree. and causes a 5-nm shift in the peak of excitation. This novel **mutation** may be useful to enhance the fluorescence properties of other GFP variants at 37.degree.. (c) 1999 Academic Press.
REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 4 OF 5 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:585457 HCAPLUS
DOCUMENT NUMBER: 129:241552
TITLE: Recombinant preparation of **green-fluorescent protein mutant** of Aequorea victoria
INVENTOR(S): Kono, Kenji; Takeda, Katsuo; Hasegawa, Mamoru
PATENT ASSIGNEE(S): Dinabeck Laboratory K. K., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 11 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 10234382	A2	19980908	JP 1997-62370	19970227

AB A **green-fluorescent protein mutant** having substitution **mutations** at 65-**Ser**.fwdarw.Thr and **147-Ser**.fwdarw.**Pro** is prepd. by expression of the **mutagenized** gene in transgenic host cells. The **mutant** is able to generate fluorescence at high temp. (37.degree.).

L8 ANSWER 5 OF 5 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:188644 HCAPLUS
DOCUMENT NUMBER: 126:260574
TITLE: A novel **mutation** which enhances the fluorescence of **green fluorescent protein** at high temperatures
AUTHOR(S): Kimata, Yukio; Iwaki, Masaharu; Lim, Chun Ren; Kohno, Kenji
CORPORATE SOURCE: Research and Education Center for Genetic Information, Nara Institute of Science and Technology, Nara, 630-01, Japan
SOURCE: Biochem. Biophys. Res. Commun. (1997), 232(1), 69-73
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English

AB **Green fluorescent protein** (**GFP**
) from Aequorea victoria is widely used as a marker of gene expression and protein localization in living cells from prokaryotes to eukaryotes. However, the total fluorescent signal from wild-type GFP is very weak when expressed in cells cultured at 37.degree. compared to 30.degree. or below. This characteristic makes GFP poorly suited to use as a marker in mammalian cells. Here the authors describe a new variant of GFP which carries a substitution of **Ser147** to **Pro** (S147P GFP) and which emits a stronger fluorescent signal than the wild-type GFP at high temp. When S147P is combined with the Ser65 to Thr **mutation** (S65T GFP), the resulting double **mutant** emits fluorescence which is several-fold stronger than GFP with a single S65T modification in both bacterial or mammalian cells. This S147P **mutation** should be useful for constructing new GFP variants which stably emit strong fluorescence at a wide range of culturing temps.

L5 6517 SEA FILE=HCAPLUS ABB=ON PLU=ON GFP(S)GREEN OR GREEN FLUORESC? PROTEIN
L6 1795 SEA FILE=HCAPLUS ABB=ON PLU=ON L5 AND (MUTAT? OR MUTAGEN? OR MUTANT OR POLYMORPH? OR POLY MORPH?)
L9 8 SEA FILE=HCAPLUS ABB=ON PLU=ON L6 AND (SER147PRO OR ((SER OR SERINE)(S)147 OR SER147 OR SERINE147)(S)(PRO OR PROLINE) OR SERINE147PROLINE OR S147P)

=> s l9 not (l2 or l8)
L10 3 L9 NOT (L2 OR L8)

L10 ANSWER 1 OF 3 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:733485 HCAPLUS
DOCUMENT NUMBER: 136:66712
TITLE: Functional correlation between the nuclear localization of Fht1p and its flocculation and heat tolerance activities in budding yeast Saccharomyces cerevisiae
AUTHOR(S): Iha, Hidekatsu; Tezuka, Hideo; Yaguchi, So-ichi; Tsurugi, Kunio
CORPORATE SOURCE: Department of Biochemistry, Yamanashi Medical University, Yamanashi, Japan
SOURCE: Journal of Biomedical Science (Basel, Switzerland) (2001), 8(5), 416-420
CODEN: JBCIEA; ISSN: 1021-7770
PUBLISHER: S. Karger AG
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Fht1p is involved in the flocculation and heat tolerance machinery of budding yeast Saccharomyces cerevisiae. Despite knowledge of its involvement in those phenotypes, a precise mechanism has yet to be discovered. To this end, the authors monitored the relationship between subcellular localization of Fht1p and its flocculation or heat tolerance function using newly developed expression vectors with a recombinant **green fluorescent protein** (**GFP**; S65T/**S147P**) of Aequorea victoria added at both the N- and C-terminus of Fht1p. The main fluorescent signal of the GFP tagged with either a wild-type Fht1p or **mutants** which preserve their flocculation function was

detected in the nucleus, whereas signals of functionless **mutants** were dispersed to the cytoplasm.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 2 OF 3 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:595996 HCAPLUS
DOCUMENT NUMBER: 133:263439
TITLE: A flexible single-step detection of blotted antigen using a fusion protein between protein A and **green fluorescent protein**
AUTHOR(S): Aoki, Takashi; Miyashita, Mamiko; Fujino, Hiroyoshi; Watabe, Hiroyuki
CORPORATE SOURCE: Department of Biochemistry, Faculty of Pharmaceutical Sciences, Health Sciences University of Hokkaido, Hokkaido, 061-0293, Japan
SOURCE: Bioscience, Biotechnology, and Biochemistry (2000), 64(7), 1547-1551
CODEN: BBBIEJ; ISSN: 0916-8451
PUBLISHER: Japan Society for Bioscience, Biotechnology, and Agrochemistry
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A **green fluorescent protein mutant** (**S147P GFP**) was fused with protein A and expressed in Escherichia coli. This fusion protein (PA-GFP147) was used in immunoblotting studies as a new detection system, designated as "flexible single-step detection (FSSD)". In FSSD, the detection of blotted antigen was done in one step, and the antigen-antibody reaction can be monitored by UV-irradn. in real time. The reaction time, therefore, can be flexibly controlled by monitoring the green fluorescence.
REFERENCE COUNT: 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 3 OF 3 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:271796 HCAPLUS
DOCUMENT NUMBER: 131:141604
TITLE: Imaging Cells in the Developing Nervous System with Retrovirus Expressing Modified **Green Fluorescent Protein**
AUTHOR(S): Okada, Ami; Lansford, Rusty; Weimann, James M.; Fraser, Scott E.; McConnell, Susan K.
CORPORATE SOURCE: Department of Biological Sciences, Stanford University, Stanford, CA, 94305, USA
SOURCE: Experimental Neurology (1999), 156(2), 394-406
CODEN: EXNEAC; ISSN: 0014-4886
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To visualize the movements of cells and their processes in developing vertebrates, we constructed replication-incompetent retroviral vectors encoding **green fluorescent**

protein (**GFP**) that can be detected as a single integrated copy per cell. To optimize GFP expression, the CMV enhancer and avian .beta.-actin promoter were incorporated within a retrovirus construct to drive transcription of red shifted (F64L, S65T) and codon-modified GFP (EGFP), EGFP tagged with GAP-43 sequences targeting the GFP to the cell membrane, or EGFP with addnl. **mutations** that increase its ability to fold properly at 37.degree. (**S147P** or V163A, S175G). We have used these viruses to efficiently mark and follow the developmental progression of a large population of cells in rat neocortex and whole avian embryos. In the chick embryo, the migration and development of GFP-marked neural crest cells were monitored using time-lapse videomicroscopy. In the neocortex, GFP clearly delineates the morphol. of a variety of neuronal and glial phenotypes. Cells expressing GFP display normal dendritic morphologies, and infected cells persist into adulthood. Cortical neurons appear to form normal local axonal and long-distance projections, suggesting that the presence of cytoplasmic or GAP-43-tagged GFP does not significantly interfere with normal development. (c) 1999 Academic Press.

REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 15:46:35 ON 07 JUN 2002)

L11 21 S L9

L12 9 DUP REM L11 (12 DUPLICATES REMOVED)

L12 ANSWER 1 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:239062 BIOSIS

DOCUMENT NUMBER: PREV200200239062

TITLE: Application of **green fluorescent protein** to affinity electrophoresis; affinity of IgG-binding domain C from streptococcal protein G to mouse IgG1.

AUTHOR(S): Kazama, Hitoshi (1); Yamada, Keiko; Aoki, Takashi; Watabe, Hiroyuki

CORPORATE SOURCE: (1) Department of Biochemistry, Faculty of Pharmaceutical Sciences, Health Sciences University of Hokkaido, 1757 Kanazawa, Ishikari-Tobetsu, Hokkaido, 061-0293: kazama@hoku-iryo-u.ac.jp Japan

SOURCE: Biological & Pharmaceutical Bulletin, (February, 2002) Vol. 25, No. 2, pp. 168-171. print. ISSN: 0918-6158.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Affinity electrophoresis (AEP) using **green fluorescent protein** (**GFP**) was studied. We constructed a fusion protein that linked S147PGFP and IgG binding domain C from streptococcal protein G (**GFP**-SpGC). The affinity of **GFP**-SpGC for mouse IgG1 was measured. The AEP using **GFP** does not require a staining step after electrophoresis, and was successful with a non-purified sample. Therefore, this method is simple and useful for measuring many samples such as those used in **mutational** studies.

L12 ANSWER 2 OF 9 WPIDS (C) 2002 THOMSON DERWENT

ACCESSION NUMBER: 2001-408713 [43] WPIDS
DOC. NO. NON-CPI: N2001-302445
DOC. NO. CPI: C2001-123795
TITLE: Bioluminescence resonance energy transfer system useful to monitor enzyme activity, comprises bioluminescent donor protein attached to first molecule and fluorescent acceptor molecule attached to second molecule.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): JOLY, E
PATENT ASSIGNEE(S): (BIOS-N) BIOSIGNAL PACKARD INC
COUNTRY COUNT: 94
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001046691	A1	20010628	(200143)*	EN	132

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2001023348	A	20010703 (200164)	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001046691	A1	WO 2000-CA1516	20001222
AU 2001023348	A	AU 2001-23348	20001222

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001023348	A	Based on	WO 200146691

PRIORITY APPLN. INFO: CA 2000-2314861 20000802; CA 1999-2291968 19991222

AN 2001-408713 [43] WPIDS

AB WO 200146691 A UPAB: 20010801

NOVELTY - A bioluminescence resonance energy transfer (BRET) system (I) comprising a bioluminescent donor protein (BDP) attached to a first molecule or modulator, and a fluorescent acceptor molecule (FAM) attached to a second molecule or modulator, where FAM can accept the energy from the BDP when they are associated, in the presence of the appropriate substrate.

DETAILED DESCRIPTION - In (I), a physical change in the modulator(s) influences the energy transfer efficiency between the BDP and the FAM, and (I) has a broad spectral resolution of at least 80 nm between the peaks of BDP and FAM emission spectra.

An INDEPENDENT CLAIM is also included for production of (I).

USE - (I) is useful to monitor protein-protein interactions or enzyme activity in vitro or in vivo (claimed). (I) is useful for in vitro and in vivo detection methods, and in assays to detect molecular changes in a wide variety of applications such as drug

discovery, analyte screening, second messenger screening, drug screening, diagnosis, genotoxicity, identification of gene function, gene discovery, and proteomics. (I) is useful to study receptor iimerization/multimerization, to characterize orphan receptors, to identify ligands for orphan receptors, for detecting interaction which occur as a consequence of receptor signaling, and to study the effect of additional molecule on receptor function.

ADVANTAGE - (I) provides an improved signal-to-base ratio (S/B) and dynamic range (DR) over a basic BRET system. (I) is readily adaptable to methods of automation and high throughput screening.

Dwg.0/34

L12 ANSWER 3 OF 9 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 2001-159852 [16] WPIDS
DOC. NO. CPI: C2001-047604
TITLE: New affinity fluorescent protein comprising a modified fluorescent protein having a heterologous amino acid sequence and a ligand-activated protein binding site, for detecting target ligand in a mixture of macromolecules or in a cell.
DERWENT CLASS: B04 D16
INVENTOR(S): EHRLICH, D J; FREYSON, Y; MATSUDAIRA, P T; ZHONG, Q
PATENT ASSIGNEE(S): (WHED) WHITEHEAD INST BIOMEDICAL RES
COUNTRY COUNT: 20
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001009177	A2	20010208	(200116)*	EN	44

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: CA JP

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001009177	A2	WO 2000-US20619	20000728

PRIORITY APPLN. INFO: US 1999-146438P 19990729
AN 2001-159852 [16] WPIDS
AB WO 200109177 A UPAB: 20010323
NOVELTY - An affinity fluorescent protein (aFP) comprising a modified fluorescent protein molecule with a **mutated** fluorescent protein molecule and a heterologous amino acid sequence having a ligand-activated protein binding site, is new.

DETAILED DESCRIPTION - A new affinity fluorescent protein (aFP) comprises a modified fluorescent protein molecule with a **mutated** fluorescent protein molecule and a heterologous amino acid sequence having a ligand-activated protein binding site. The modified fluorescent protein molecule displays an altered spectral property when the binding site is engaged with ligand relative to the spectral property displayed when the binding site is not engaged by ligand.

INDEPENDENT CLAIMS are also included for the following:

(1) an aFP expression cassette or expression vector comprising a modified **green fluorescent protein** (**GFP**) nucleic acid sequence which is **mutated** and

operatively linked to expression control sequences, where the modified **GFP** sequence comprises a recombinant peptide having restriction endonuclease sites introduced at a location of the **GFP** molecule selected from between Gln 157 and Lys 158, Glu 172 and Asp 173, or both locations;

(2) a host cell comprising a recombinant nucleic acid having expression control sequences operatively linked to a nucleotide sequence encoding an aFP, which has a modified or **mutated** GFP molecule and a heterologous amino acid sequence functioning as a ligand-activated protein binding site, and which displays an altered spectral property when the binding site is engaged with ligand relative to the spectral property displayed when the binding site is not engaged by ligand;

(3) detecting the presence of a target ligand in a mixture of macromolecules by:

(a) contacting a sample with an aFP comprising a binding site for the target ligand;

(b) exciting the aFP with light; and

(c) measuring the fluorescent property that differs as a result of ligand activation of the aFP; and

(4) detecting the occurrence of a target ligand in a cell by:

(a) introducing into the cell an aFP comprising a binding site for the target ligand;

(b) exciting the aFP present in the cell with light; and

(c) detecting the fluorescence pattern due to ligand activation of the affinity fluorescent protein in the cell and comparing it to the fluorescence pattern in a control cell, where the fluorescence pattern determines the occurrence of the target ligand in the cell.

USE - The aFP is useful for:

(i) detecting target ligand in a mixture of macromolecules or in a cell;

(ii) for detecting and monitoring a range of in vitro and in vivo biological activities which include specific molecular processes in cells, cellular physiology, and the detection, quantification and/or purification of a target ligand from a wide variety of samples; and

(iii) use as a substitute for reporter-molecule labeled monoclonal or polyclonal antibodies.

The aFP can covalently bind a variety of molecules (e.g. natural, synthetic, biological, non-biological, organic, inorganic, protein, non-protein small or large), and can function both as molecular recognition groups and as molecular biosensors which are capable of sensing and reporting the interaction of a binding site with its cognate ligand.

Dwg.0/11

L12 ANSWER 4 OF 9 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2001500401 MEDLINE
DOCUMENT NUMBER: 21434002 PubMed ID: 11549884
TITLE: Functional correlation between the nuclear localization of Fht1p and its flocculation and heat tolerance activities in budding yeast Saccharomyces cerevisiae.
AUTHOR: Iha H; Tezuka H; Yaguchi S; Tsurugi K
CORPORATE SOURCE: Department of Biochemistry, Yamanashi Medical University, Yamanashi, Japan.. hiha@swallow.res.yamanashi-med.ac.jp
SOURCE: JOURNAL OF BIOMEDICAL SCIENCE, (2001 Sep) 8 (5)

416-20.
Journal code: 9421567. ISSN: 1021-7770.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20010911
Last Updated on STN: 20020124
Entered Medline: 20011231

AB Fht1p is involved in the flocculation and heat tolerance machinery of budding yeast Saccharomyces cerevisiae. Despite knowledge of its involvement in those phenotypes, a precise mechanism has yet to be discovered. To this end, we monitored the relationship between subcellular localization of Fht1p and its flocculation or heat tolerance function using newly developed expression vectors with a recombinant **green fluorescent protein** (**GFP**; S65T/**S147P**) of Aequorea victoria added at both the N- and C-terminus of Fht1p. The main fluorescent signal of the **GFP** tagged with either a wild-type Fht1p or **mutants** which preserve their flocculation function was detected in the nucleus, whereas signals of functionless **mutants** were dispersed to the cytoplasm.

L12 ANSWER 5 OF 9 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001051448 MEDLINE
DOCUMENT NUMBER: 20399378 PubMed ID: 10945281
TITLE: A flexible single-step detection of blotted antigen using a fusion protein between protein A and **green fluorescent protein**
.
AUTHOR: Aoki T; Miyashita M; Fujino H; Watabe H
CORPORATE SOURCE: Department of Biochemistry, Faculty of Pharmaceutical Sciences, Health Sciences University of Hokkaido, Ishikari-Tobetsu, Japan.. aokit@hoku-iryo-u.ac.jp
SOURCE: BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, (2000 Jul) 64 (7) 1547-51.
Journal code: BDP. ISSN: 0916-8451.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200012
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001212

AB A **green fluorescent protein** **mutant** (**S147P GFP**) was fused with protein A and expressed in Escherichia coli. This fusion protein (PA-GFP147) was used in immunoblotting studies as a new detection system, designated as "flexible single-step detection (FSSD)". In FSSD, the detection of blotted antigen was done in one step, and the antigen-antibody reaction can be monitored by UV-irradiation in real time. The reaction time, therefore, can be flexibly controlled by monitoring the **green** fluorescence.

L12 ANSWER 6 OF 9 BIOSIS

ACCESSION NUMBER: 2000:369249 BIOSIS
DOCUMENT NUMBER: PREV200000369249
TITLE: **S147P green fluorescent protein**: A less thermosensitive **green fluorescent protein** variant.
AUTHOR(S): Kimata, Yukio (1); Ren Lim, Chun; Kohno, Kenji
CORPORATE SOURCE: (1) Research and Education Center for Genetic Information, Nara Institute of Science and Technology, Ikoma, Nara, 630-01 Japan
SOURCE: Conn, P. Michael. Methods in Enzymology, (1999) Vol. 302, pp. 373-378. Methods in Enzymology; Green fluorescent protein. print.
Publisher: Academic Press Inc. 525 B Street, Suite 1900, San Diego, CA, 92101-4495, USA.
ISSN: 0076-6879. ISBN: 0-12-182203-6 (cloth).
DOCUMENT TYPE: Book
LANGUAGE: English
SUMMARY LANGUAGE: English

L12 ANSWER 7 OF 9 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 1999263448 MEDLINE
DOCUMENT NUMBER: 99263448 PubMed ID: 10328944
TITLE: Imaging cells in the developing nervous system with retrovirus expressing modified **green fluorescent protein**.
AUTHOR: Okada A; Lansford R; Weimann J M; Fraser S E; McConnell S K
CORPORATE SOURCE: Department of Biological Sciences, Stanford University, Stanford, California, 94305, USA.. amio@leland.stanford.edu
CONTRACT NUMBER: EY08411 (NEI)
MH49176 (NIMH)
NS12151 (NINDS)
+
SOURCE: EXPERIMENTAL NEUROLOGY, (1999 Apr) 156 (2) 394-406.
Journal code: EQF; 0370712. ISSN: 0014-4886.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990614
Last Updated on STN: 19990614
Entered Medline: 19990603

AB To visualize the movements of cells and their processes in developing vertebrates, we constructed replication-incompetent retroviral vectors encoding **green fluorescent protein** (**GFP**) that can be detected as a single integrated copy per cell. To optimize **GFP** expression, the CMV enhancer and avian beta-actin promoter were incorporated within a retrovirus construct to drive transcription of redshifted (F64L, S65T) and codon-modified **GFP** (EGFP), EGFP tagged with GAP-43 sequences targeting the **GFP** to the cell membrane, or EGFP with additional **mutations** that increase its ability to fold properly at 37 degrees C (**S147P** or V163A, S175G). We have used these viruses to efficiently mark and follow the developmental progression of a large population of cells in rat neocortex and whole avian embryos. In the chick embryo, the

migration and development of **GFP**-marked neural crest cells were monitored using time-lapse videomicroscopy. In the neocortex, **GFP** clearly delineates the morphology of a variety of neuronal and glial phenotypes. Cells expressing **GFP** display normal dendritic morphologies, and infected cells persist into adulthood. Cortical neurons appear to form normal local axonal and long-distance projections, suggesting that the presence of cytoplasmic or GAP-43-tagged **GFP** does not significantly interfere with normal development.

L12 ANSWER 8 OF 9 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 1999137259 EMBASE
TITLE: **S147P green fluorescent protein**: A less thermosensitive **green fluorescent protein** variant.
AUTHOR: Kimata Y.; Chu Ren Lim; Kohno K.
CORPORATE SOURCE: Y. Kimata, Res./Educ. Center for Genetic Info., Nara Institute of Science/Technology, Ikoma, Nara 630-01, Japan
SOURCE: Methods in Enzymology, (1999) 302/- (373-378).
ISSN: 0076-6879 CODEN: MENZAU
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English

L12 ANSWER 9 OF 9 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 97236282 MEDLINE
DOCUMENT NUMBER: 97236282 PubMed ID: 9125154
TITLE: A novel **mutation** which enhances the fluorescence of **green fluorescent protein** at high temperatures.
AUTHOR: Kimata Y; Iwaki M; Lim C R; Kohno K
CORPORATE SOURCE: Research and Education Center for Genetic Information, Nara Institute of Science and Technology, Japan.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997 Mar 6) 232 (1) 69-73.
Journal code: 9Y8; 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970506
Last Updated on STN: 19980206
Entered Medline: 19970422

AB **Green fluorescent protein** (**GFP**) from Aequorea victoria is widely used as a marker of gene expression and protein localization in living cells from prokaryotes to eukaryotes. However, the total fluorescent signal from wild-type **GFP** is very weak when expressed in cells cultured at 37 degrees C compared to 30 degrees C or below. This characteristic makes **GFP** poorly suited to use as a marker in mammalian cells. Here we describe a new variant of **GFP** which carries a substitution of **Ser147** to **Pro** (**S147P GFP**) and which emits a stronger fluorescent signal than the

wild-type **GFP** at high temperature. When **S147P** is combined with the Ser65 to Thr **mutation** (S65T **GFP**), the resulting double **mutant** emits fluorescence which is several-fold stronger than **GFP** with a single S65T modification in both bacterial or mammalian cells. This **S147P mutation** should be useful for constructing new **GFP** variants which stably emit strong fluorescence at a wide range of culturing temperatures.

FILE 'HOME' ENTERED AT 15:47:43 ON 07 JUN 2002